```
           1       10        20        30        40        50        60        70        80        90       100
           |--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
    human  MRPQGPAASPQRLRGL--LLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKGEKGECLRESF
    mouse  MHPQGRAAPPQLLLGLFLVLLLLLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESF
rice_fish              MTPLSPRLLILLCLALPLHGQE--KGRSRGYRKDPDADKF--GSCLQGPAGTPGRDGNPGANGIPGTPGIPGRDGLKGEKGECVSEVF
ebra_fish              MGTKLTQLLICFWISLPFCVTQKAKERIPRQ-RDAEFTDKYQA-CVQGVPGVQGRDGNPGINGIPGTPGIPGRDGLKGEKGECVSERF
  chicken                                              RPREVLEAYNGVCLQGPSGVPGRDGNPGTNGIPGTPGIPGRDGPKGEKGECLRESI
  nsensus  ...................ll......p......k.......r.r#v...yng.ClQGp.GvpGRDGnPG.NGIPGTPGIPGRDG.KGEKGEClrEsf

           101    110       120       130       140       150       160       170       180       190       200
           |--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
    human  EESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVE
    mouse  EESWTPNYKQCSWSSLNTGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPELNSTINIHRTSSVE
rice_fish  EEPWKPNYKQCAWNSLNYGIDLGKIADCTFTKLRSESALRVLFTGSLRLKCKEACCQRWYFTFDGAECTGPLPVESIIYLNQGSPELNSTINIHRTSSVE
ebra_fish  EEPWKPNFKQCAWNSLNYGIDLGKIAECTFTKQRSDSALRVLFSGSLRLKCKTACCQRWYFTFNGAECTGPLPIESIVYLDQGSPELNSTINIHRTSTVE
  chicken  EESWTPNFKQCSWSALNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRSACCQRWYFTFNGAECAGPLPIEAIIYLDQGSPELNSTINIHRTSSVE
  nsensus  EEsWtPN%KQCsWssLNYGIDLGKIA#CTFTKnRS#SALRVLFsGSLRLKCr.ACCQRWYFTF#GAEC.GPLP!EaI!YL#QGSPE$NSTINIHRTSsVE

           201    210       220       230       240  245
           |--------|---------|---------|---------|----|
    human  GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
    mouse  GLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
rice_fish  GLCEGIKAGLVDVALWVGTCADYPRGDASTGWNSVSRIIIEELPK
ebra_fish  GLCEGIHAGLVDVGIWVGTCADYPRGDASTGWNSVSRVIIEELPK
  chicken  GLCEGINAGLVDIAIWVGTCSDYPRGDASTGWNSVSRIIIEELPK
  nsensus  GLCEGI.AGLVD!aiWVGTCsDYPrGDASTGWNSVSR!IIEELPK
```

FIG._1

```
         10        20        30        40        50
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNG
     60        70        80        90       100
MCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNY
   110       120       130       140       150
KQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYF
0        170       180       190       200       210
TFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVA
      220       230       240
IWVGTCSDYPKGDASTGWNSVSRIIIEELPK
```

FIG._2

BEST AVAILABLE COPY

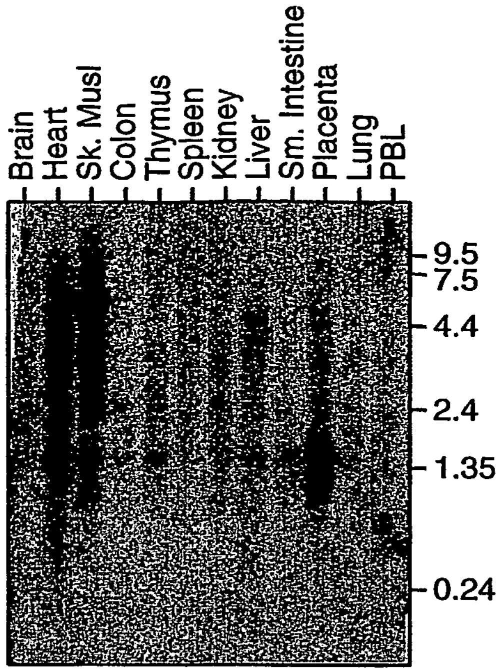

Brain
Heart
Sk. Musl
Colon
Thymus
Spleen
Kidney
Liver
Sm. Intestine
Placenta
Lung
PBL
9.5
7.5
4.4
2.4
1.35
0.24

FIG._3A

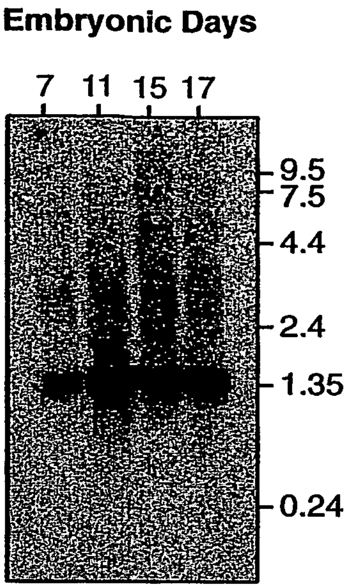

Embryonic Days
7
11
15
17
9.5
7.5
4.4
2.4
1.35
0.24

FIG._3B

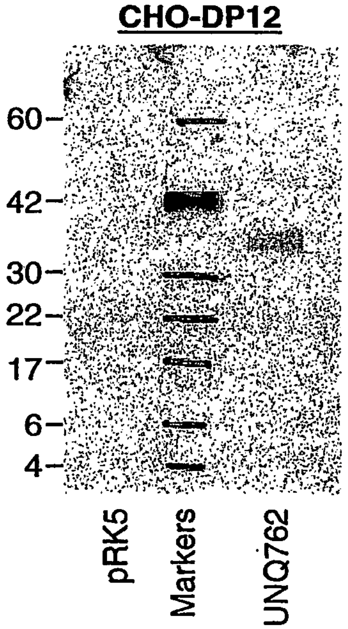

CHO-DP12
60
42
30
22
17
6
4
pRK5
Markers
UNQ762

FIG._4A

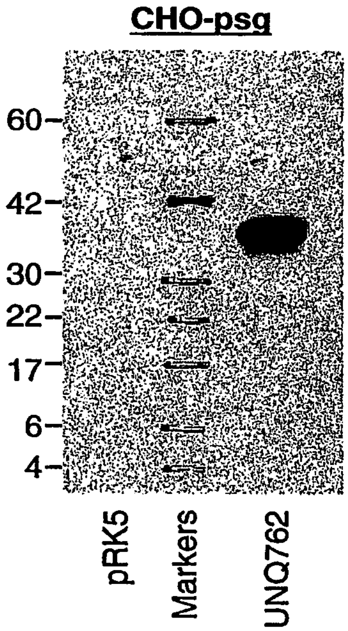

CHO-psg
60
42
30
22
17
6
4
pRK5
Markers
UNQ762

FIG._4B

FIG._5A

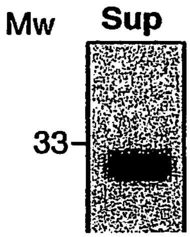
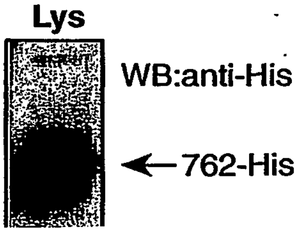


FIG._5B


Lys
WB:anti-His
762-His

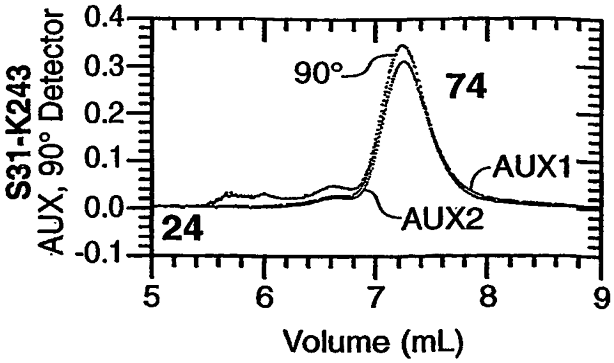


FIG._6A

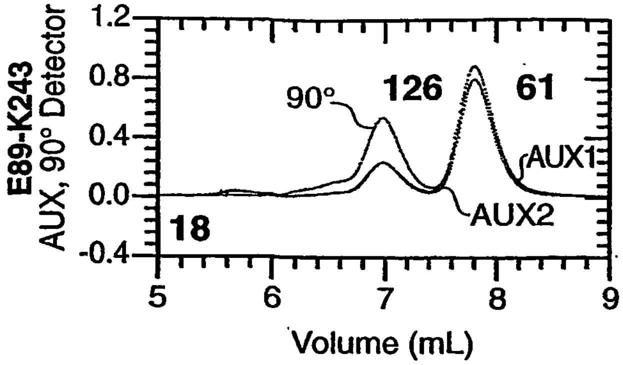


FIG._6B

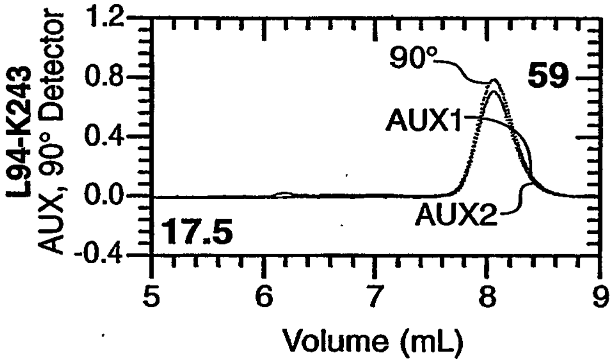


FIG._6C

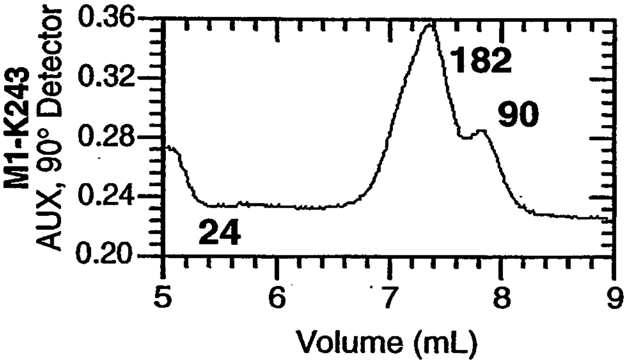


FIG._7A

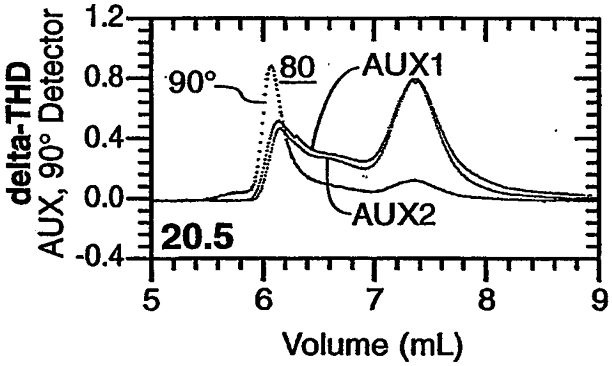


FIG._7B

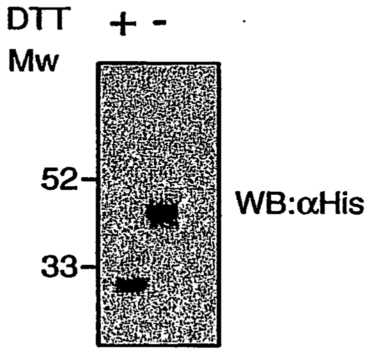

DTT
+
-
Mw
52
33
WB:αHis

FIG._7C

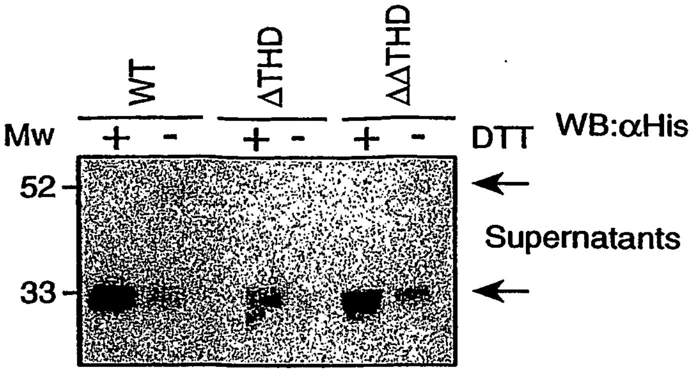


FIG._8A

WT
ΔTHD
ΔΔTHD
Mw
+ - + - + -
DTT
WB:αHis
52
33
Supernatants

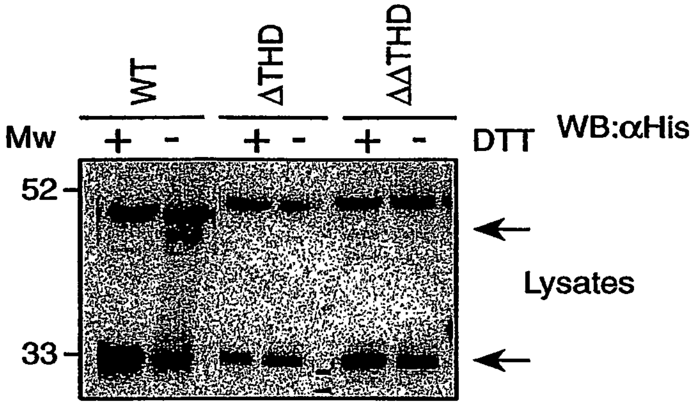


FIG._8B

WT
ΔTHD
ΔΔTHD
Mw
+ - + - + -
DTT
WB:αHis
52
33
Lysates

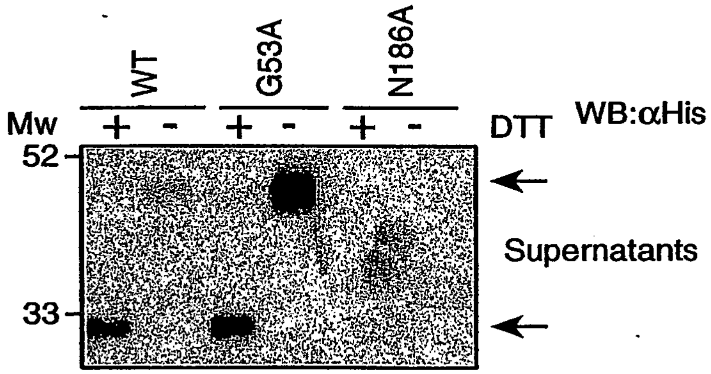


FIG._9A

WT
G53A
N186A
Mw
+ - + - + -
DTT
WB:αHis
52
33
Supernatants

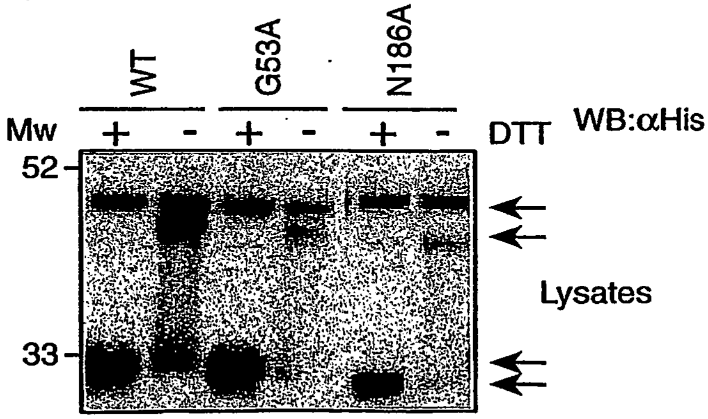


FIG._9B

WT
G53A
N186A
Mw
+ - + - + -
DTT
WB:αHis
52
33
Lysates

FIG._10A

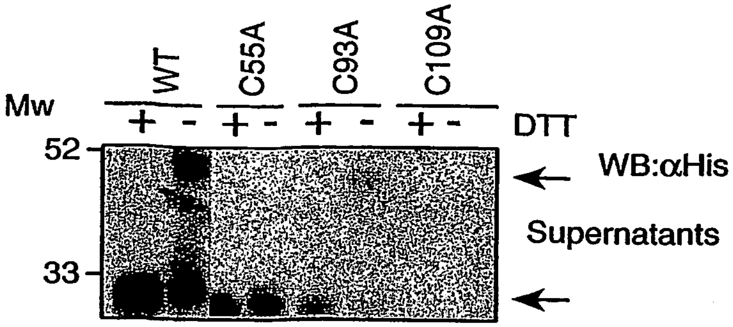

WT
C55A
C93A
C109A
Mw
+ - + - + - + -
DTT
52
33
WB:αHis
Supernatants

FIG._10B

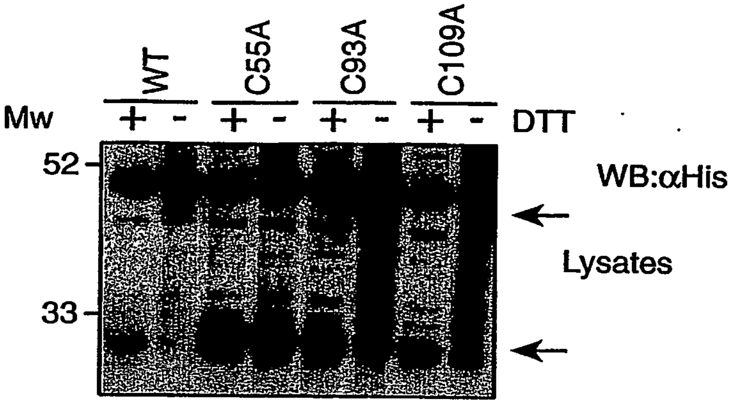
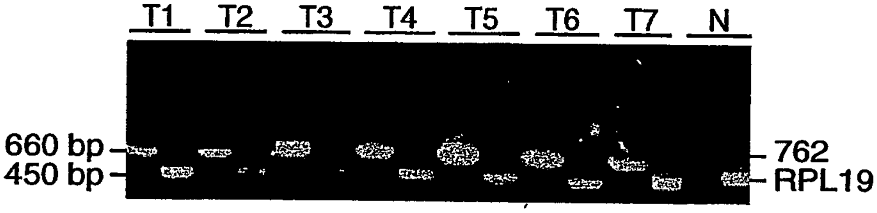

WT
C55A
C93A
C109A
Mw
+ - + - + - + -
DTT
52
33
WB:αHis
Lysates

FIG._11


T1
T2
T3
T4
T5
T6
T7
N
660 bp
450 bp
762
RPL19

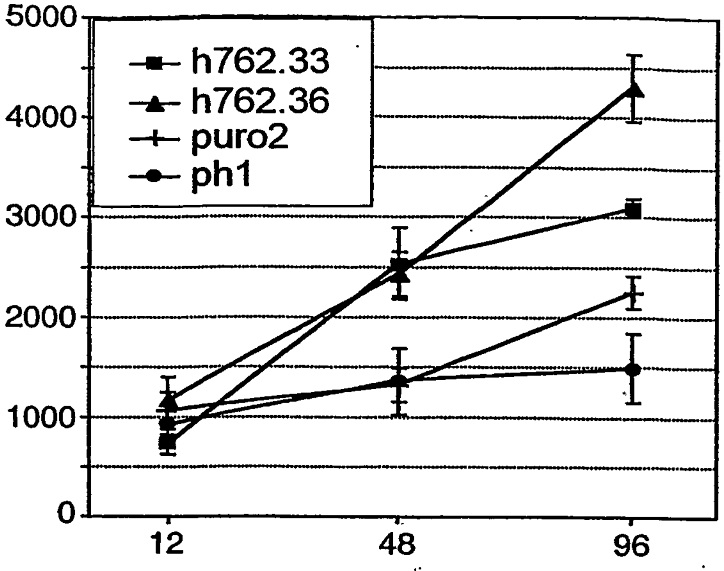


FIG._12A

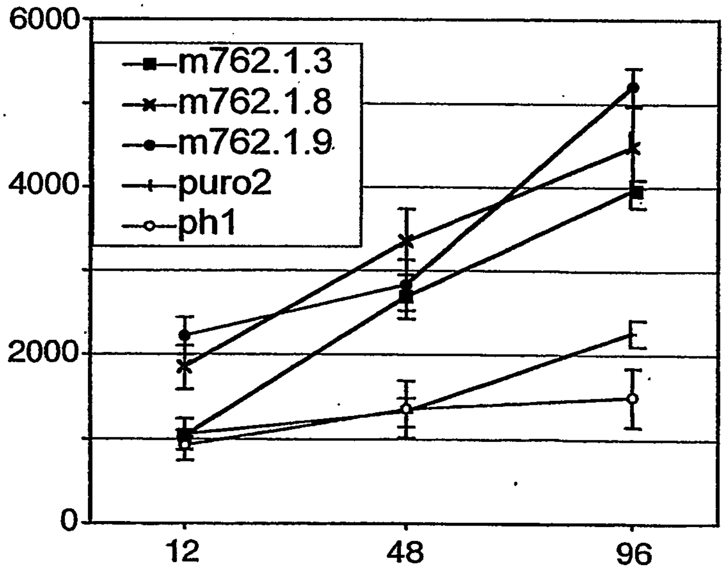


FIG._12B

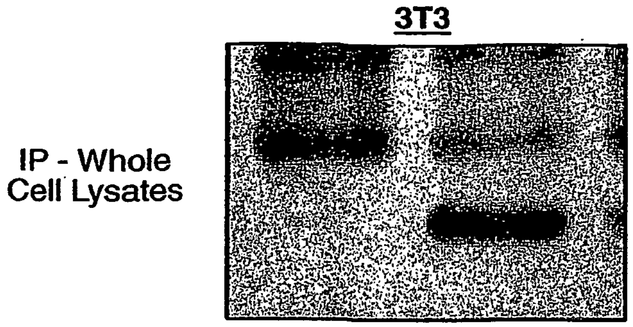

3T3
IP - Whole Cell Lysates

FIG._13A

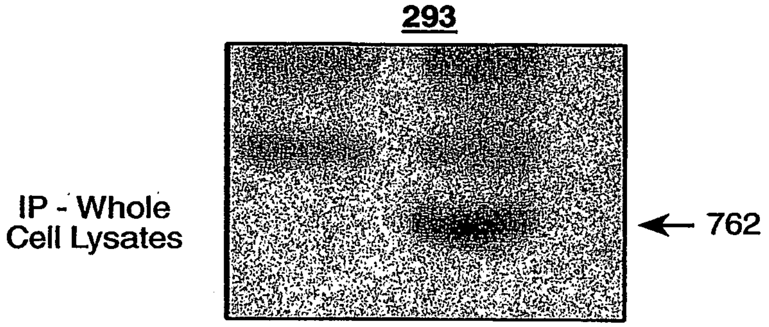

293
IP - Whole Cell Lysates
762

FIG._13B

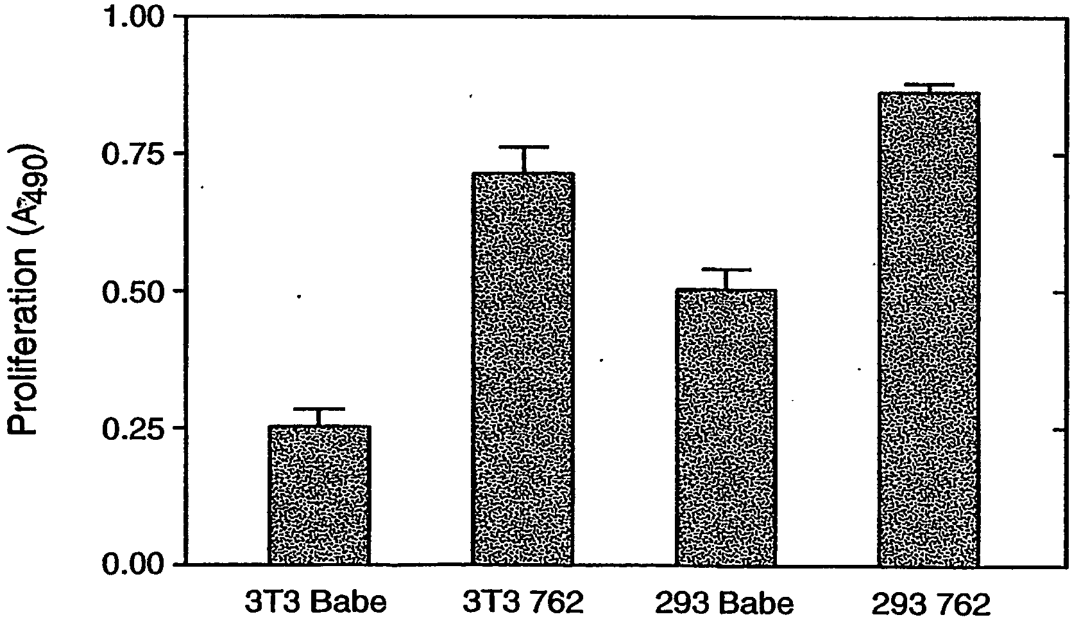


FIG._13C

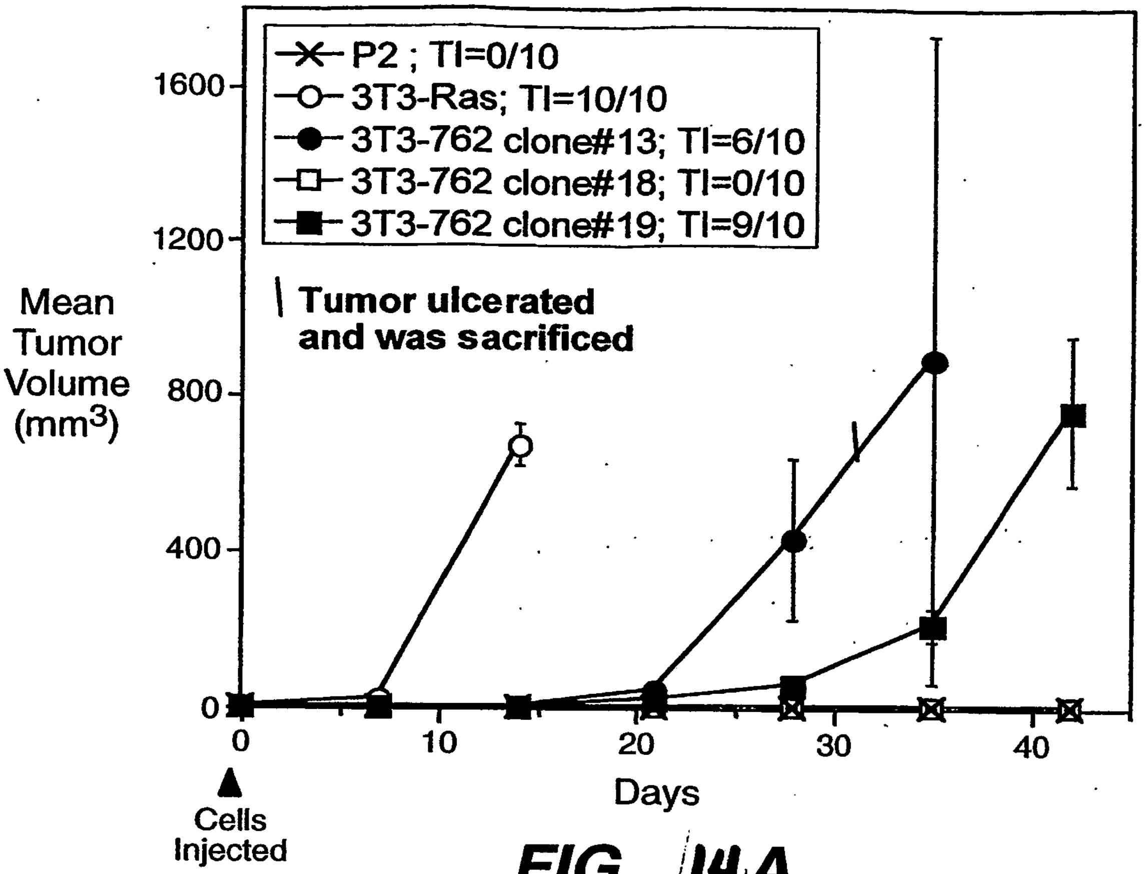


FIG._14A

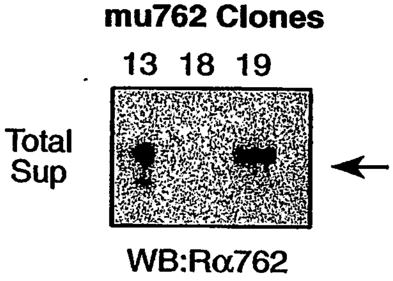

mu762 Clones
13 18 19
Total Sup
WB:Rα762

FIG._14B

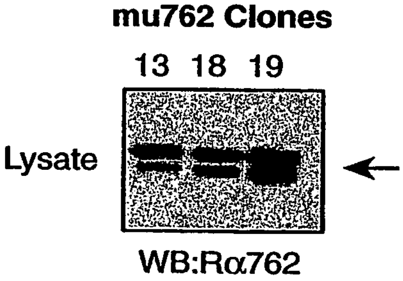

mu762 Clones
13 18 19
Lysate
WB:Rα762

FIG._14C

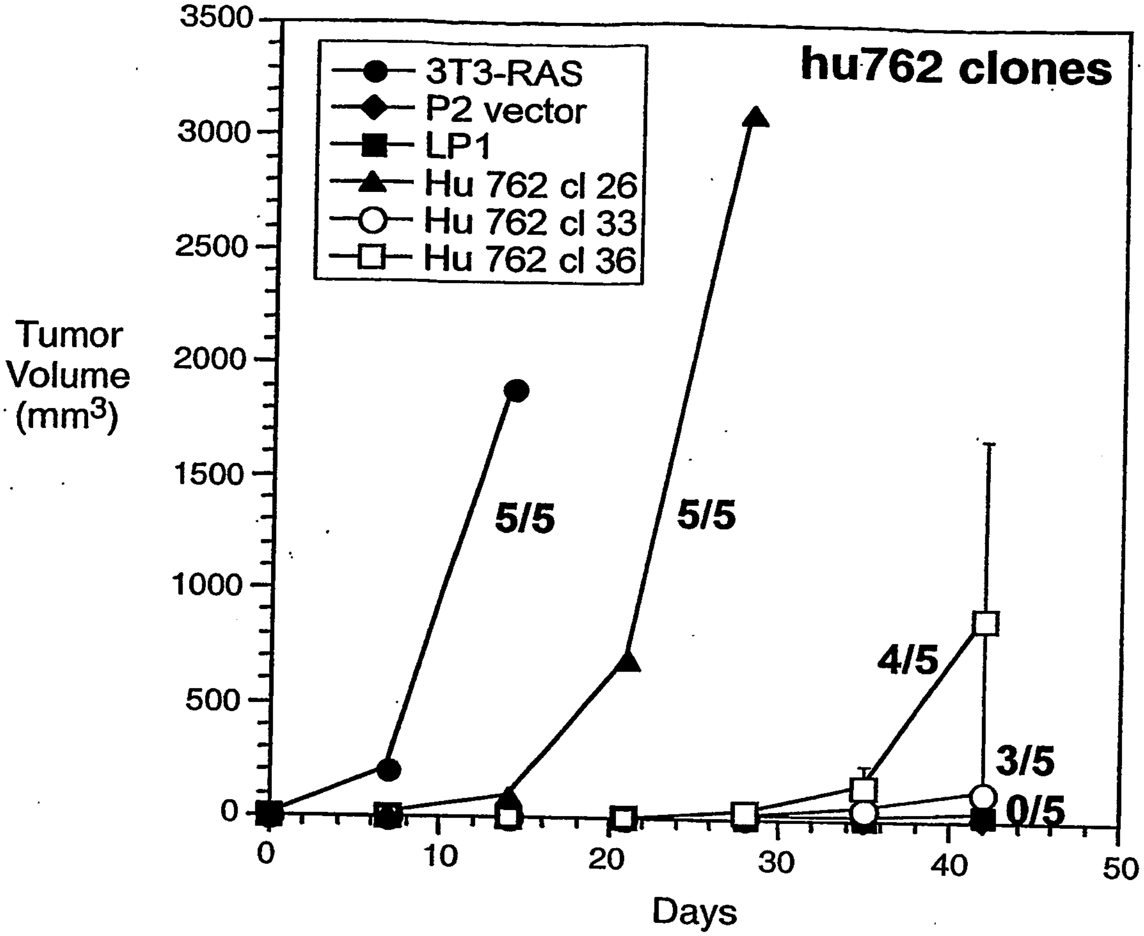

3500
3000
2500
2000
1500
1000
500
0
Tumor Volume (mm³)
0
10
20
30
40
50
Days
3T3-RAS
P2 vector
LP1
Hu 762 cl 26
Hu 762 cl 33
Hu 762 cl 36
hu762 clones
5/5
5/5
4/5
3/5
0/5

FIG._15

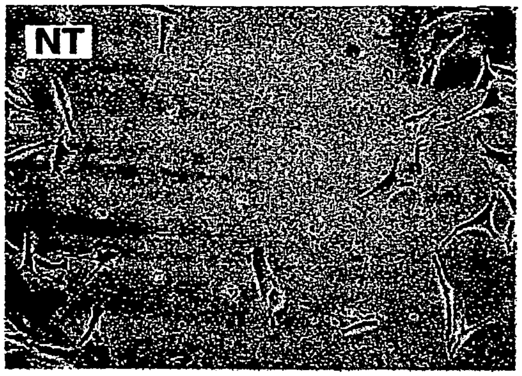


FIG._16A

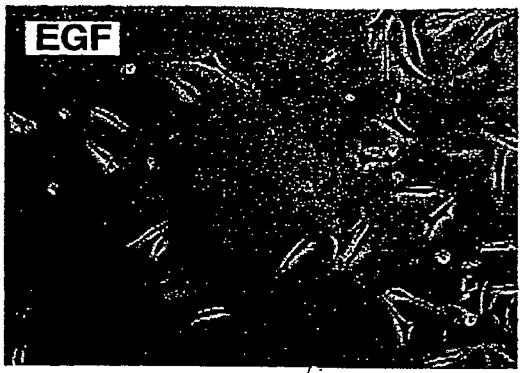


FIG._16C

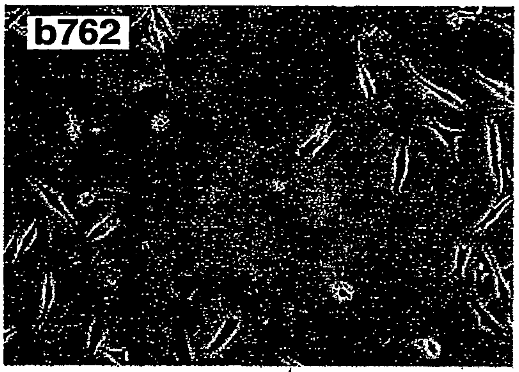


FIG._16B

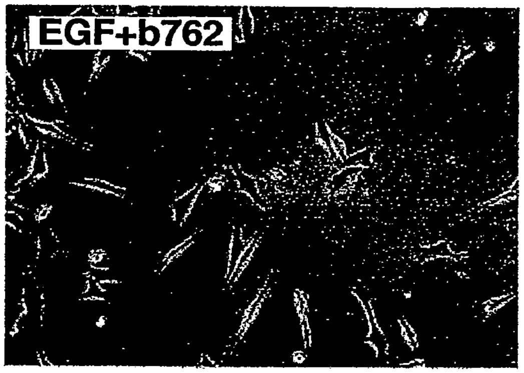


FIG._16D

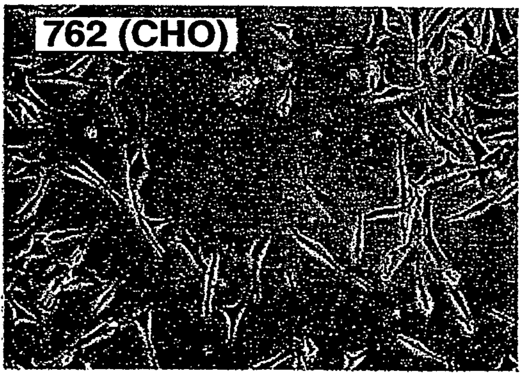


FIG._16E

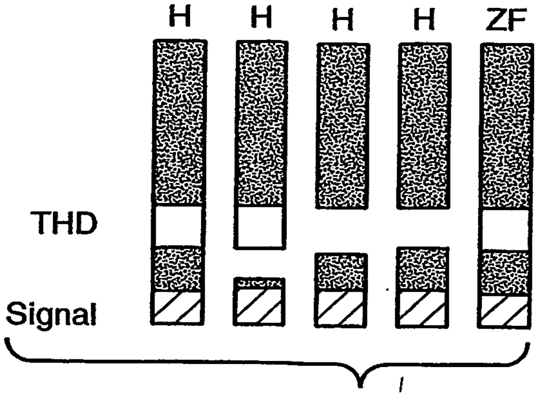

H
H
H
H
ZF
THD
Signal

FIG._17A

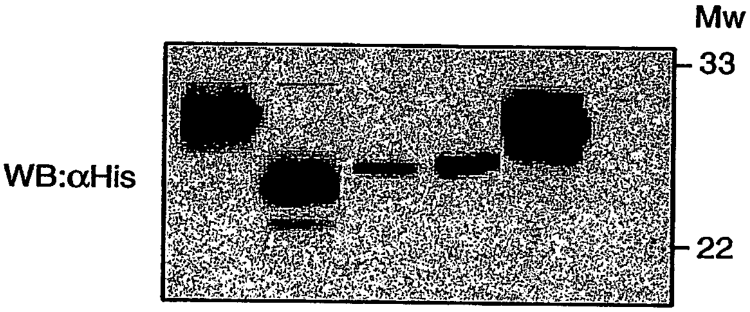

Mw
33
22
WB:αHis

FIG._17B

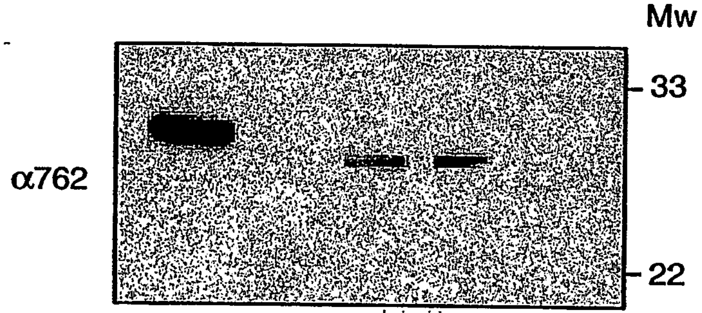

Mw
33
22
α762

FIG._17C

HI						H2											H3															
8	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102	Name
.	I	S	G	S	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	L	-	F	D	Y	S7
.	I	T	N	S	D	A	T	I	Y	P	Y	G	G	Y	T	Y	C	A	R	G	G	G	M	D	G	Y	V	M	D	Y	S16
.	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F5
.	I	N	N	Y	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F6
.	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	S4
.	I	S	N	Y	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y	S9
.	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F13
.	I	S	G	S	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F47

FIG._18

	Phage		Fab			IgG	
	762 S/S	762 F/F	762 S/S	762 F/S	762 F/F	762 S/S	762 F/F
S4	3nM	0.9nM	3.6nM (1.9nM)	32nM	13.4nM	0.5nM	3.1nM
	762 S/S	762 F/F	762 S/S	762 F/S	762 F/F	762 S/S	762 F/F
S7	35nM	2.7nM	113nM	57nM	n/a	7.3nM	41nM

FIG._21

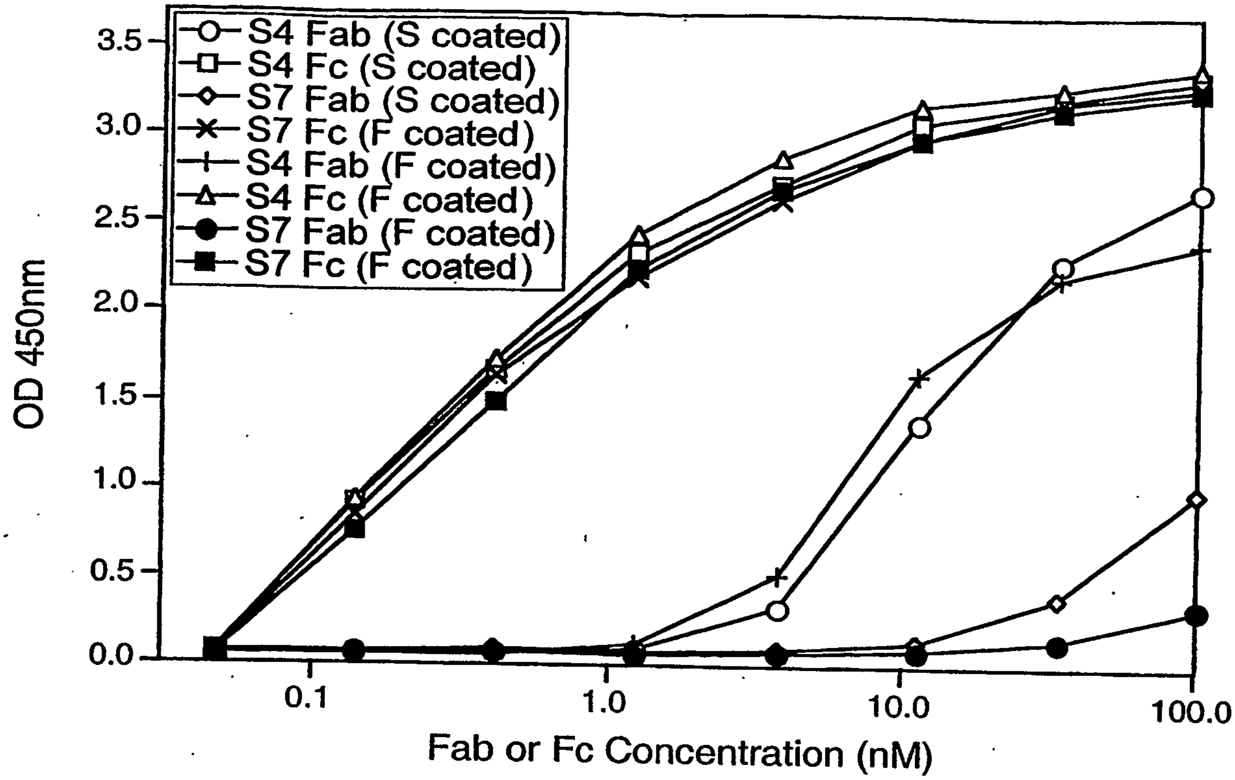

S4 Fab (S coated)
S4 Fc (S coated)
S7 Fab (S coated)
S7 Fc (F coated)
S4 Fab (F coated)
S4 Fc (F coated)
S7 Fab (F coated)
S7 Fc (F coated)
OD 450nm
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.1
1.0
10.0
100.0
Fab or Fc Concentration (nM)

FIG._19

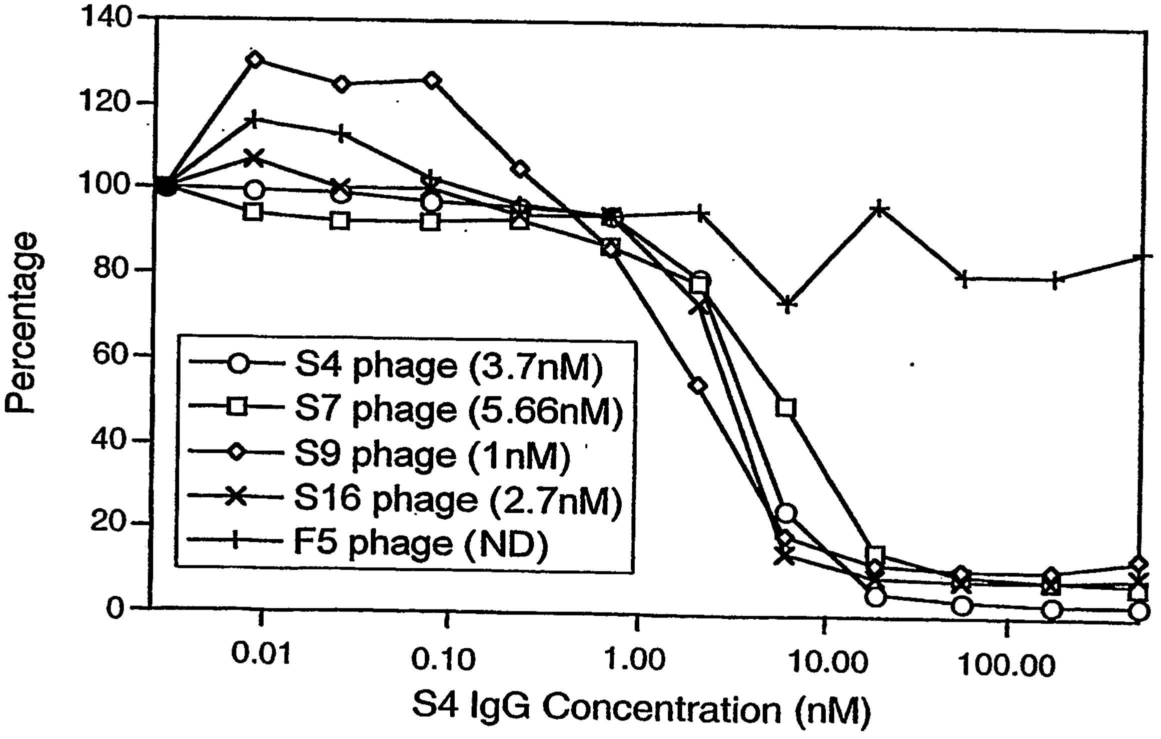

140
120
100
80
60
40
20
0
Percentage
S4 phage (3.7nM)
S7 phage (5.66nM)
S9 phage (1nM)
S16 phage (2.7nM)
F5 phage (ND)
0.01
0.10
1.00
10.00
100.00
S4 IgG Concentration (nM)

FIG._22

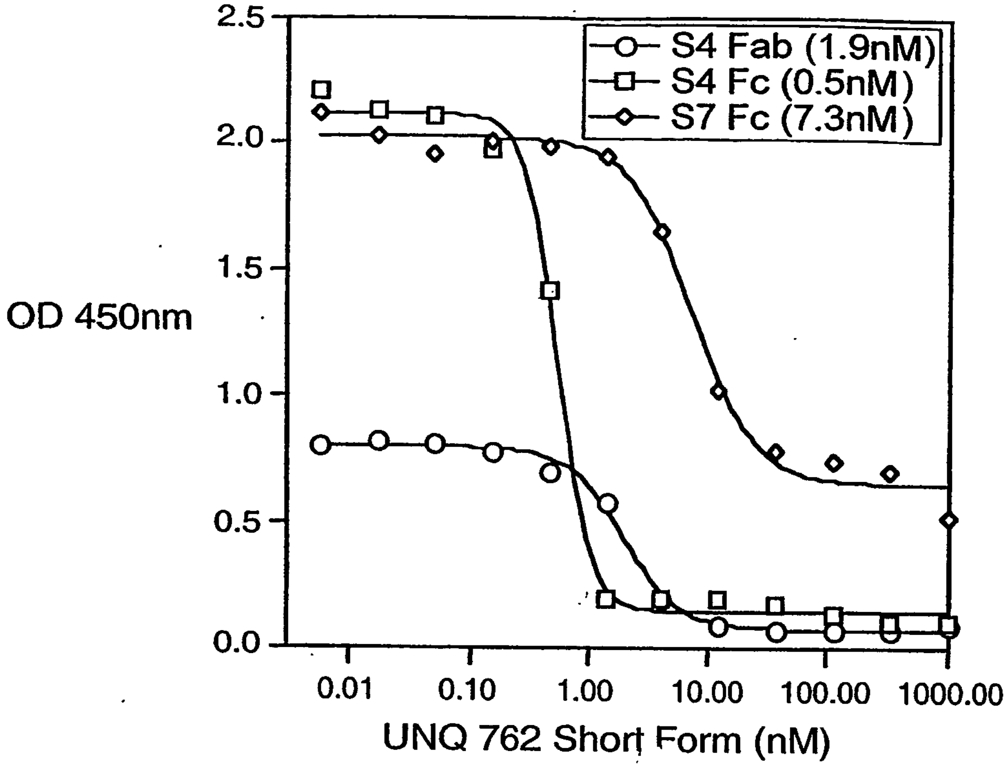


FIG._20 A.

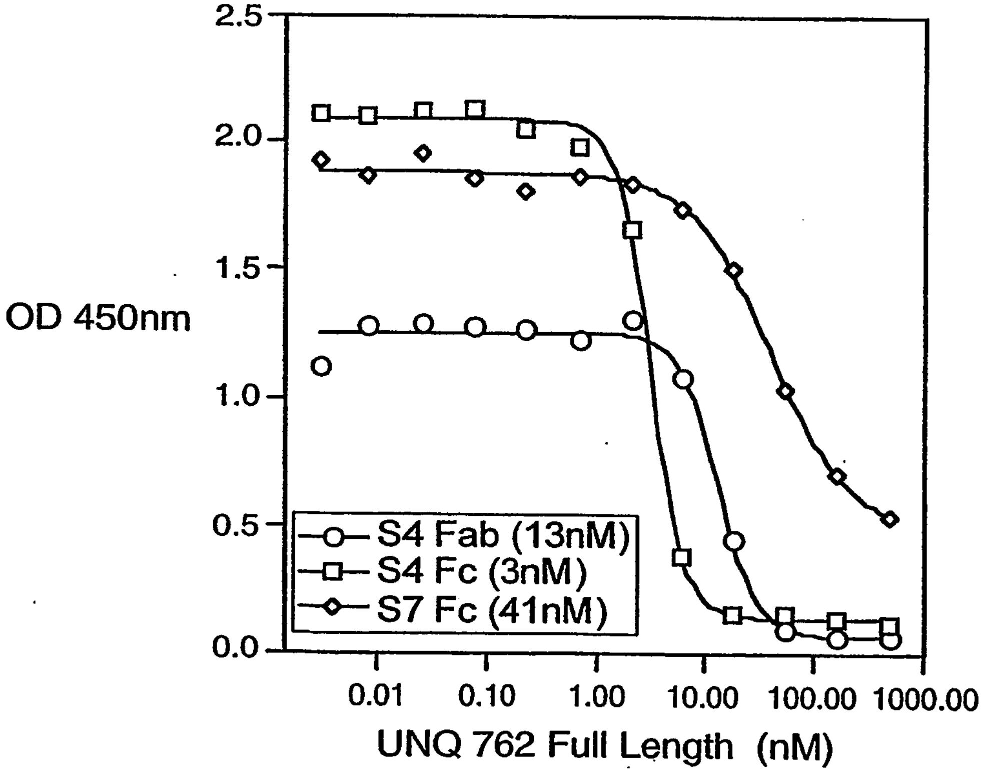


FIG._20B

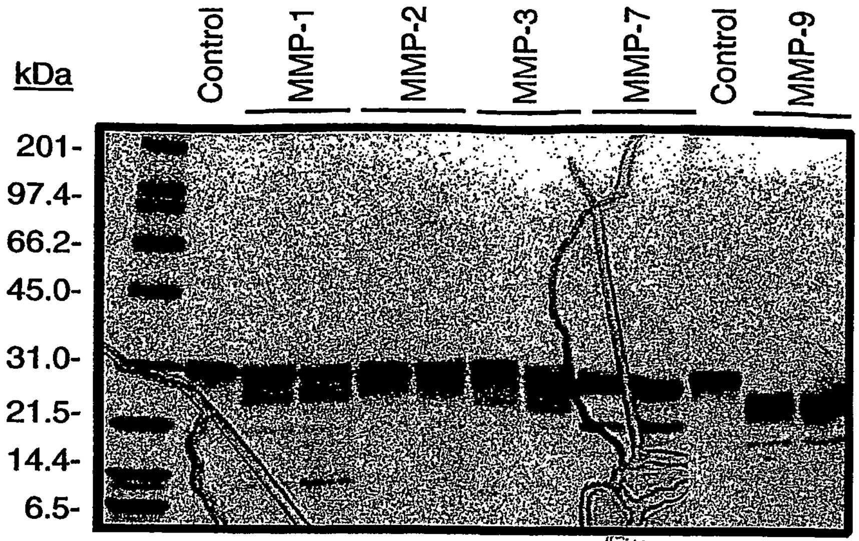

kDa
Control
MMP-1
MMP-2
MMP-3
MMP-7
Control
MMP-9
201-
97.4-
66.2-
45.0-
31.0-
21.5-
14.4-
6.5-

FIG._23

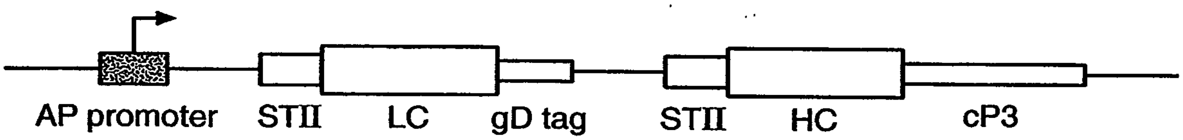

AP promoter
STII
LC
gD tag
STII
HC
cP3

FIG._24A

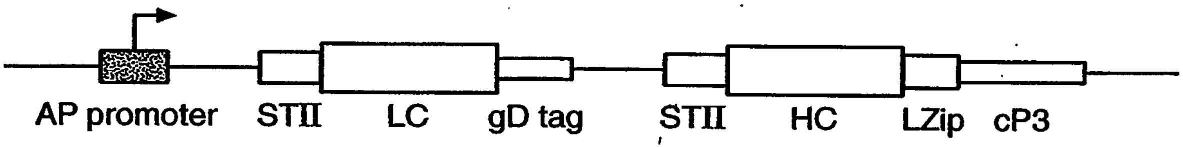

AP promoter
STII
LC
gD tag
STII
HC
LZip
cP3

FIG._24B

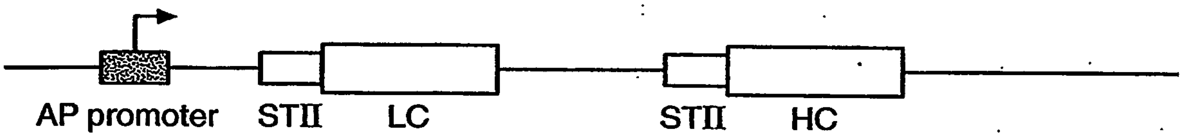

AP promoter
STII
LC
STII
HC

FIG._24C

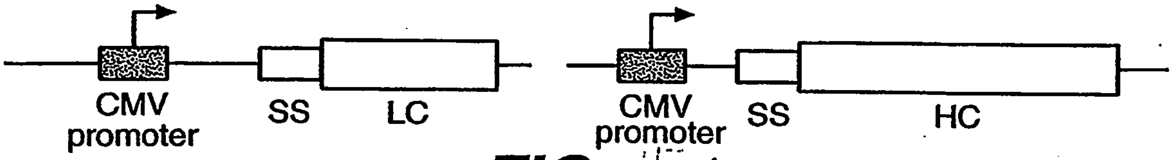

CMV promoter
SS
LC
CMV promoter
SS
HC

FIG._24D

```
  1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTTATG AAAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCGTTT TTTCTATTGC TACAAATGCC
    AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAAATAC TTTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
  1                                             M  K  K  N  I   A  F  L   L  A  S   M  F  V  F   S  I  A   T  N  A
                                              ^start of stII signal sequence
                                              ^met

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCCTCTGT GGGCGATAGG GTCACCATCA CCTGCCGTGC CAGTCAGGAT GTGTCCACTG
    ATACGTCTAT AGGTCTACTG GGTCAGGGGC TCGAGGGACA GGCGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCACG GTCAGTCCTA CACAGGTGAC
 22 Y  A  D  I   Q  M  T   Q  S  P   S  S  L  S   A  S  V   G  D  R   V  T  I  T   C  R  A   S  Q  D   V  S  T  A
       ^start of light chain                                                            ^CDR-L1

601 CTGTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCCTCTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
    GACATCGGAC CATAGTTGTC TTTGGTCCTT TTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
 56  V  A  W   Y  Q  Q   K  P  G  K   A  P  K   L  L  I   Y  S  A  S   F  L  Y   S  G  V   P  S  R  F   S  G  S
                                                          ^CDR-L2

701 CGGTTCCGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTC
    GCCAAGGCCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGGTGCAAG
 89 G  S  G   T  D  F  T   L  T  I   S  S  L   Q  P  E  D   F  A  T   Y  Y  C   Q  Q  S  Y   T  T  P   P  T  F
                                                                            ^CDR-L3
```

FIG._ 25A

```
301 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
    CCTGTCCCAT GGTTCCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
122 G  Q  G  T   K  V  E   I  K  R   T  V  A  A   P  S  V   F  I  F   P  P  S  D   E  Q  L   K  S  G   T  A  S  V

901 TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA
    AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG AGGGTCCTCT CACAGTGTCT
156  V  C  L   L  N  N   F  Y  P  R   E  A  K   V  Q  W   K  V  D  N   A  L  Q   S  G  N   S  Q  E  S   V  T  E

01 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT
   CGTCCTGTCG TTCCTGTCGT GGATGTCGGA GTCGTCGTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA
89  Q  D  S   K  D  S  T   Y  S  L   S  S  T   L  T  L  S   K  A  D   Y  E  K   H  K  V  Y   A  C  E   V  T  H

01 CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGCGGT AAGGACCTGG
   GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTCGAGG CCATACCGAC TAGGCTTGGC AAAGGCGCCA TTCCTGGACC
22 Q  G  L  S   S  P  V   T  K  S   F  N  R  G   E  C  G   A  S  S   G  M  A  D   P  N  R   F  R  G   K  D  L  A
                                                                  ^end of light chain, start of gD tag

01 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
   GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCCA TTGATCTCCA ACTCCACTAA AATACTTTTT
56  O
23

                                                                                                      M  K  K
                                                                                                      ^start of stII

01 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGCGTACGC TGAGGTTCAG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG
   CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACGTC
20  N  I  A   F  L  L  A   S  M  F   V  F  S   I  A  T  N   A  Y  A   E  V  Q   L  V  E  S   G  G  G   L  V  Q
                                                                  ^start of heavy chain

01 CCAGGGGGCT CACTCCGTTT GTCCTGTGCA GCTTCTGGCT TCAACATTAA AGACACCTAT ATACACTGGG TGCGTCAGGC CCCGGGTAAG GGCCTGGAAT
   GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
14 P  G  G  S   L  R  L   S  C  A   A  S  G  F   N  I  K   D  T  Y   I  H  W  V   R  Q  A   P  G  K   G  L  E  W
                                     ^CDR-H1
```

FIG._ 25B

```
1501 GGGTTGCAAG GATTTATCCT ACGAATGGTT ATACTAGATA TGCCGATAGC GTCAAGGGCC GTTTCACTAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA
     CCCAACGTTC CTAAATAGGA TGCTTACCAA TATGATCTAT ACGGCTATCG CAGTTCCCGG CAAAGTGATA TTCGCGTCTG TGTAGGTTTT TGTGTCGGAT
  48  V  A  R  I  Y  P  T  N  G  Y  T  R  Y  A  D  S  V  K  G  R  F  T  I  S  A  D  T  S  K  N  T  A  Y
          ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTA GCCGCTGGGG AGGGGACGGC TTCTATGCTA TGGACTACTG GGGTCAAGGA
     GGATGTTTAC TTGTCGAATT CTCGACTCCT GTGACGGCAG ATAATAACAT CGGCGACCCC TCCCCTGCCG AAGATACGAT ACCTGATGAC CCCAGTTCCT
  81 L  Q  M  N  S  L  R  A  E  D  T  A  V  Y  Y  C  S  R  W  G  G  D  G  F  Y  A  M  D  Y  W  G  Q  G
                                                         ^CDR-H3

1701 ACACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT
     TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGGG GGACCGTGGG AGGAGGTTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA
 114 T  L  V  T  V  S  S  A  S  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C

1801 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC
     CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG
 148  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S

1901 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG
     TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC
 181  G  L  Y  S  L  S  S  V  V  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K

2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC ACCTCAGTGG CGGTGGCTCT GGTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA
     CAGCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTTGAG TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGCGAT
 214 V  D  K  K  V  E  P  K  S  C  D  K  T  H  L  S  G  G  G  S  G  S  G  D  F  D  Y  E  K  M  A  N  A  N
                                               ^end of heavy chain
                                                 ^start of gene III coat protein (267-end)

2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGCGCT ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA
     TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTTGCGCGA TGTCAGACTG CGATTTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT
 248  K  G  A  M  T  E  N  A  D  E  N  A  L  Q  S  D  A  K  G  K  L  D  S  V  A  T  D  Y  G  A  A  I  D
```

FIG._25c

```
2201 TGGTTTCATT GGTGACGTTT CCGGCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT
     ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAAACG ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA
 281 G  F  I  G  D  V  S  G  L  A  N  G  N  G  A  T  G  D  F  A  G  S  N  S  Q  M  A  Q  V  G  D  G  D

2301 AATTCACCTT TAATGAATAA TTTCCGTCAA TATTTACCTT CCCTCCCTCA ATCGGTTGAA TGTCGCCCTT TTGTCTTTAG CGCTGGTAAA CCATATGAAT
     TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA GGGAGGGAGT TAGCCAACTT ACAGCGGGAA AACAGAAATC GCGACCATTT GGTATACTTA
 314 N  S  P  L  M  N  N  F  R  Q  Y  L  P  S  L  P  Q  S  V  E  C  R  P  F  V  F  S  A  G  K  P  Y  E  F

2401 TTTCTATTGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT CTTTGCGTTT CTTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT
     AAAGATAACT AACACTGTTT TATTTGAATA AGGCACCACA GAAACGCAAA GAAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA
 348  S  I  D  C  D  K  I  N  L  F  R  G  V  F  A  F  L  L  Y  V  A  T  F  M  Y  V  F  S  T  F  A  N  I

2501 ACTGCGTAAT AAGGAGTCTT AATCATGCCA GTTCTTTTGG CTAGCGCCGC CCTATACCTT GTCTGCCTCC CCGCGTTGCG TCGCGGTGCA TGGAGCCGGG
     TGACGCATTA TTCCTCAGAA TTAGTACGGT CAAGAAAACC GATCGCGGCG GGATATGGAA CAGACGGAGG GGCGCAACGC AGCGCCACGT ACCTCGGCCC
 381 L  R  N  K  E  S  O

2601 CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGCGCAA
     GGTGGAGCTG GACTTACCTT CGGCCGCCGT GGAGCGATTG CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAACG CCTCTTGACA CTTACGCGTT

2701 ACCAACCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT CCAGCAGCCG CACGCGGCGC ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCGCATGA
     TGGTTGGGAA CCGTCTTGTA TAGGTAGCGC AGGCGGTAGA GGTCGTCGGC GTGCGCCGCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT

2801 TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGGG TTGCCTTACT GGTTAGCAGA ATGAATCACC GATACGCGAG CGAACGTGAA GCGACTGCTG
     AGCACGAGGA CAGCAACTCC TGGGCCGATC CGACCGCCCC AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC

2901 CTGCAAAACG TCTGCGACCT GAGCAACAAC ATGAATGGTC TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATTATG
     GACGTTTTGC AGACGCTGGA CTCGTTGTTG TACTTACCAG AAGCCAAAGG CACAAAGCAT TTCAGACCTT TGCGCCTTCA GTCGCGGGAC GTGGTAATAC

3001 TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCTGTG GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATT TTTCTCTGGT
     AAGGCCTAGA CGTAGCGTCC TACGACGACC GATGGGACAC CTTGTGGATG TAGACATAAT TGCTTCGCGA CCGTAACTGG GACTCACTAA AAAGAGACCA
```

FIG._25D

```
101 CCCGCCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT
    GGGCGGCGTA GGTATGGCGG TCAACAAATG GGAGTGTTGC AAGGTCATTG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA

201 CATCGGTATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA CACGGAGGCA TCAAGTGACC AAACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA
    GTAGCCATAG TAATGGGGGT ACTTGTCTTT AAGGGGGAAT GTGCCTCCGT AGTTCACTGG TTTGTCCTTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT

301 GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT GGACGCGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA
    CTTCGGTCTG TAATTGCGAA GACCTCTTTG AGTTGCTCGA CCTGCGCCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGCGAC TACTCGAAAT

401 CCGCAGGATC CGGAAATTGT AAACGTTAAT ATTTTGTTAA AATTCGCGTT AAATTTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA
    GGCGTCCTAG GCCTTTAACA TTTGCAATTA TAAAACAATT TTAAGCGCAA TTTAAAAACA ATTTAGTCGA GTAAAAAATT GGTTATCCGG CTTTAGCCGT

501 AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT GAGTGTTGTT CCAGTTTGGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA
    TTTAGGGAAT ATTTAGTTTT CTTATCTGGC TCTATCCCAA CTCACAACAA GGTCAAACCT TGTTCTCAGG TGATAATTTC TTGCACCTGA GGTTGCAGTT

 01 AGGGCGAAAA ACCGTCTATC AGGGCTATGG CCCACTACGT GAACCATCAC CCTAATCAAG TTTTTTGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC
    TCCCGCTTTT TGGCAGATAG TCCCGATACC GGGTGATGCA CTTGGTAGTG GGATTAGTTC AAAAAACCCC AGCTCCACGG CATTTCGTGA TTTAGCCTTG

701 CCTAAAGGGA GCCCCCGATT TAGAGCTTGA CGGGGAAAGC CGGCGAACGT GGCGAGAAAG GAAGGGAAGA AAGCGAAAGG AGCGGGCGCT AGGGCGCTGG
    GGATTTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTCG GCCGCTTGCA CCGCTCTTTC CTTCCCTTCT TTCGCTTTCC TCGCCCGCGA TCCCGCGACC

801 CAAGTGTAGC GGTCACGCTG CGCGTAACCA CCACACCCGC CGCGCTTAAT GCGCCGCTAC AGGGCGCGTC CGGATCCTGC CTCGCGCGTT TCGGTGATGA
    GTTCACATCG CCAGTGCGAC GCGCATTGGT GGTGTGGGCG GCGCGAATTA CGCGGCGATG TCCCGCGCAG GCCTAGGACG GAGCGCGCAA AGCCACTACT

 01 CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT
    GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG TGTCGAACAG ACATTCGCCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGCG CAGTCGCCCA

 01 GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATACT GGCTTAACTA TGCGGCATCA GAGCAGATTG TACTGAGAGT
    CAACCGCCCA CAGCCCCGCG TCGGTACTGG GTCAGTGCAT CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA
```

FIG._25E

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4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATGCGTAAGG AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
     CGTGGTATAC GCCACACTTT ATGGCGTGTC TACGCATTCC TCTTTTATGG CGTAGTCCGC GAGAAGGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG

4201 GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC
     CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCCGCC ATTATGCCAA TAGGTGTCTT AGTCCCCTAT TGCGTCCTTT CTTGTACACT CGTTTTCCGG

4301 AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG
     TCGTTTTCCG GTCCTTGGCA TTTTTCCGGC GCAACGACCG CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTGCGA GTTCAGTCTC

4401 GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG
     CACCGCTTTG GGCTGTCCTG ATATTTCTAT GGTCCGCAAA GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG ACGGCGAATG GCCTATGGAC

4501 TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC
     AGGCGGAAAG AGGGAAGCCC TTCGCACCGC GAAAGAGTAT CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACACG

4601 ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC
     TGCTTGGGGG GCAAGTCGGG CTGGCGACGC GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTC TGTGCTGAAT AGCGGTGACC GTCGTCGGTG

4701 TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC
     ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG

4801 TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC
     ACGCGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCG

4901 AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT
     TCGTCTAATG CGCGTCTTTT TTTCCTAGAG TTCTTCTAGG AAACTAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA

5001 GGTCATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC
     CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA AATTTAATTT TTACTTCAAA ATTTAGTTAG ATTTCATATA TACTCATTTG AACCAGACTG
```

FIG._25F

```
5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC
     TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG

5201 GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC
     CCCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG

5301 CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC
     GCTCGCGTCT TCACCAGGAC GTTGAAATAG GCGGAGGTAG GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCG

5401 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT
     TTGCAACAAC GGTAACGACG TCCGTAGCAC CACAGTGCGA GCAGCAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA

5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT
     GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA

5601 GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT
     CGTATTAAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGGTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA

5701 TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA
     ACGAGAACGG GCCGCAGTTG TGCCCTATTA TGGCGCGGTG TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTTGAGAGTT

5801 GGATCTTACC GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTCACC AGCGTTTCTG GGTGAGCAAA
     CCTAGAATGG CGACAACTCT AGGTCAAGCT ACATTGGGTG AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAAGAC CCACTCGTTT

5901 AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG
     TTGTCCTTCC GTTTTACGGC GTTTTTTCCC TTATTCCCGC TGTGCCTTTA CAACTTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAAATAGTC

6001 GGTTATTGTC TCATGAGCGG ATACATATTT GAATGTATTT AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG AAAAGTGCCA CCTGACGTCT
     CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA TCTTTTTATT TGTTTATCCC CAAGGCGCGT GTAAAGGGGC TTTTCACGGT GGACTGCAGA
```

FIG._25G

```
101 AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG
    TTCTTTGGTA ATAATAGTAC TGTAATTGGA TATTTTTATC CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC

201 AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGCT CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT
    TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCAAAGGTGA

301 TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC AGTAGAAAGG GCTTCATCAT ATCAAATGCA ACGTACAAAG AAATAGGGCT TCTGACCTGT
    ACTGTGAAAC TAGGGACTAC CTTTTGCGTA TTAGACCCTG TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTTATCCCGA AGACTGGACA

401 GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAAACTATC TCACACATCG ACAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAAT
    CTTCGTTGTC AGTTACCCGT AAACATATTC TGTTTGATAG AGTGTGTAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAAG CATCTCTACA TGTCACTTTA

501 CCCCGAAATT ATACACATGA CTGAAGGAAG GGAGCTCGTC ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC
    GGGGCTTTAA TATGTGTACT GACTTCCTTC CCTCGAGCAG TAAGGGACGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTTTCAA AGGTGAACTG

 01 ACTTTGATCC CTGATGGAAA ACGCATAATC TGGGACAGTA GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAGAAAT AGGGCTTCTG ACCTGTGAAG
    TGAAACTAGG GACTACCTTT TGCGTATTAG ACCCTGTCAT CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTTTCTTTA TCCCGAAGAC TGGACACTTC

701 CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAAATCC
    GTTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAAGCA TCTCTACATG TCACTTTAGG

801 CCGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTTACTTTA AAAAAGTTTC CACTTGACAC
    GGCTTTAATA TGTGTACTGA CTTCCTTCCC TCGAGCAGTA AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACTGTG

 01 TTTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTAGA AAGGGCTTCA TCATATCAAA TGCAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA
    AAACTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCATCT TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCGT

 01 ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC ATCGACAAAC CAATACAATC
    TGTCAGTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG TAGCTGTTTG GTTATGTTAG
```

FIG._ 25H

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   1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTTATG AAAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCGTTT TTTCTATTGC TACAAATGCC
     AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAAATAC TTTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
   1                                          M   K  K  N   I  A  F  L   L  A  S   M  F  V   F  S  I  A   T  N  A
                                              ^start of stII sequence

 501 TATGCATCCG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA
     ATACGTAGGC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT
  22   Y  A  S   D  I  Q  M   T  Q  S   P  S  S   L  S  A  S   V  G  D   R  V  T   I  T  C  R   A  S  Q   D  V  S T
         ^light chain start                                                                 ^CDR-L1

 601 CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG
     GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC
  56     A  V  A   W  Y  Q   Q  K  P   G  K  A  P   K  L  L   I  Y  S   A  S  F  L   Y  S  G   V  P  S   R  F  S  G
                                                                   ^CDR-L2

 701 TAGCGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAT CTTATACTAC TCCTCCCACG
     ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTA GAATATGATG AGGAGGGTGC
  89    S  G  S   G  T  D   F  T  L  T   I  S  S   L  Q  P   E  D  F  A   T  Y  Y   C  Q  Q   S  Y  T  T   P  P  T
                                                                                      ^CDR-L3
```

FIG._ 26A

```
1 TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCCT
  AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA
2 F  G  Q  G   T  K  V   E  I  K   R  T  V  A   A  P  S   V  F  I   F  P  P  S   D  E  Q   L  K  S   G  T  A  S

1 CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTCAC
  GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG
6  V  V  C   L  L  N   N  F  Y  P   R  E  A   K  V  Q   W  K  V  D   N  A  L   Q  S  G   N  S  Q  E   S  V  T

1 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC
  TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
9  E  Q  D   S  K  D  S   T  Y  S   L  S  S   T  L  T  L   S  K  A   D  Y  E   K  H  K  V   Y  A  C   E  V  T

1 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC
  GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG
2 H  Q  G  L   S  S  P   V  T  K   S  F  N  R   G  E  C   G  A  S   S  G  M  A   D  P  N   R  F  R   G  K  D  L
                                                                   ^end of light chain, start of gD tag

1 TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTAACTAGA GGTTGAGGTG ATTTTATGAA
  ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC ACCGGGATCA TGCGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAAATACTT
6   A  O
3
                                                                                                            M  K
                                                                                                            ^start of stII

1 AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG
  TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC
1  K  N  I   A  F  L  L   A  S  M   F  V  F   S  I  A  T   N  A  Y   A  E  V   Q  L  V  E   S  G  G   G  L  V
                                                                     ^start of heavy chain

1 CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG GCTTCAACAT TAAAGACACC TATATACACT GGGTGCGTCA GGCCCCGGGT AAGGGCCTGG
  GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC CGAAGTTGTA ATTTCTGTGG ATATATGTGA CCCACGCAGT CCGGGGCCCA TTCCCGGACC
3 Q  P  G  G   S  L  R   L  S  C   A  A  S  G   F  N  I   K  D  T   Y  I  H  W   V  R  Q   A  P  G   K  G  L  E
                                            ^CDR-H1
```

FIG._ 26B

```
1501 AATGGGTTGC AAGGATTTAT CCTACGAATG GTTATACTAG ATATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC
     TTACCCAACG TTCCTAAATA GGATGCTTAC CAATATGATC TATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCGCGT CTGTGTAGGT TTTTGTGTCG
  47  W  V  A   R  I  Y   P  T  N  G   Y  T  R   Y  A  D   S  V  K  G   R  F  T   I  S  A   D  T  S  K   N  T  A
           ^CDR-H2

1601 CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC GTCTATTATT GTAGCCGCTG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA
     GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG CAGATAATAA CATCGGCGAC CCCTCCCCTG CCGAAGATAC GATACCTGAT GACCCCAGTT
  80  Y  L  Q   M  N  S  L   R  A  E   D  T  A   V  Y  Y  C   S  R  W   G  G  D   G  F  Y  A   M  D  Y   W  G  Q
                                                                 ^CDR-H3

1701 GGAACACTAG TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG
     CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC
 113 G  T  L  V   T  V  S   S  A  S   T  K  G  P   S  V  F   P  L  A   P  S  S  K   S  T  S   G  G  T   A  A  L  G

1801 GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC
     CGACGGACCA GTTCCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG
 147  C  L  V   K  D  Y   F  P  E  P   V  T  V   S  W  N   S  G  A  L   T  S  G   V  H  T   F  P  A  V   L  Q  S

1901 CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC
     GAGTCCTGAG ATGAGGGAGT CGTCGCACCA CTGGCACGGG AGGTCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG
 180  S  G  L   Y  S  L  S   S  V  V   T  V  P   S  S  S  L   G  T  Q   T  Y  I   C  N  V  N   H  K  P   S  N  T

2001 AAGGTCGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACGGCCG CATGAAACAG CTAGAGGACA AGGTCGAAGA GCTACTCTCC AAGAACTACC
     TTCCAGCTGT TCTTTCAACT CGGGTTTAGA ACACTGTTTT GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG
 213 K  V  D  K   K  V  E   P  K  S   C  D  K  T   H  G  R   M  K  Q   L  E  D  K   V  E  E   L  L  S   K  N  Y  H
                                                          ^end of heavy chain, start of leucine zipper

2101 ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTCGG GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAAGAT
     TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC CCTCGCGCCT TTCGAATCAC CGCCACCGAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA
 247  L  E  N   E  V  A   R  L  K  K   L  V  G   E  R  G   K  L  S  G   G  G  S   G  S  G   D  F  D  Y   E  K  M
   end of leucine zipper, start of gene III coat protein (267-end)^
```

FIG._26C

```
2201 GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC TACAGTCTGA CGCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTACGGT
     CCGTTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA CTTTTGCGCG ATGTCAGACT GCGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA
 280 A N A  N K G A  M T E  N A D  E N A L  Q S D  A K G  K L D S  V A T  D Y G

2301 GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG
     CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC GATTACCATT ACCACGATGA CCACTAAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAGC
 313 A A I D  G F I  G D V  S G L A  N G N  G A T  G D F A  G S N  S Q M  A Q V G

2401 GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA
     CACTGCCACT ATTAAGTGGA AATTACTTAT TAAAGGCAGT TATAAATGGA AGGGAGGGAG TTAGCCAACT TACAGCGGGA AAACAGAAAT CGCGACCATT
 347  D G D  N S P  L M N N  F R Q  Y L P  S L P Q  S V E  C R P  F V F S  A G K

2501 ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG
     TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAAT AAGGCACCAC AGAAACGCAA AGAAAATATA CAACGGTGGA AATACATACA TAAAAGATGC
 380 P Y E  F S I D  C D K  I N L  F R G V  F A F  L L Y  V A T F  M Y V  F S T

2601 TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAATCATGCC AGTTCTTTTG GCTAGCGCCG CCCTATACCT TGTCTGCCTC CCCGCGTTGC GTCGCGGTGC
     AAACGATTGT ATGACGCATT ATTCCTCAGA ATTAGTACGG TCAAGAAAAC CGATCGCGGC GGGATATGGA ACAGACGGAG GGGCGCAACG CAGCGCCACG
 413 F A N I  L R N  K E S  O

2701 ATGGAGCCGG GCCACCTCGA CCTGAATGGA AGCCGGCGGC ACCTCGCTAA CGGATTCACC ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAACTG
     TACCTCGGCC CGGTGGAGCT GGACTTACCT TCGGCCGCCG TGGAGCGATT GCCTAAGTGG TGAGGTTCTT AACCTCGGTT AGTTAAGAAC GCCTCTTGAC

2801 TGAATGCGCA AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC GCACGCGGCG CATCTCGGGC AGCGTTGGGT CCTGGCCACG
     ACTTACGCGT TTGGTTGGGA ACCGTCTTGT ATAGGTAGCG CAGGCGGTAG AGGTCGTCGG CGTGCGCCGC GTAGAGCCCG TCGCAACCCA GGACCGGTGC

2901 GGTGCGCATG ATCGTGCTCC TGTCGTTGAG GACCCGGCTA GGCTGGCGGG GTTGCCTTAC TGGTTAGCAG AATGAATCAC CGATACGCGA GCGAACGTGA
     CCACGCGTAC TAGCACGAGG ACAGCAACTC CTGGGCCGAT CCGACCGCCC CAACGGAATG ACCAATCGTC TTACTTAGTG GCTATGCGCT CGCTTGCACT

3001 AGCGACTGCT GCTGCAAAAC GTCTGCGACC TGAGCAACAA CATGAATGGT CTTCGGTTTC CGTGTTTCGT AAAGTCTGGA AACGCGGAAG TCAGCGCCCT
     TCGCTGACGA CGACGTTTTG CAGACGCTGG ACTCGTTGTT GTACTTACCA GAAGCCAAAG GCACAAAGCA TTTCAGACCT TTGCGCCTTC AGTCGCGGGA
```

FIG._26D

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3101 GCACCATTAT GTTCCGGATC TGCATCGCAG GATGCTGCTG GCTACCCTGT GGAACACCTA CATCTGTATT AACGAAGCGC TGGCATTGAC CCTGAGTGAT
     CGTGGTAATA CAAGGCCTAG ACGTAGCGTC CTACGACGAC CGATGGGACA CCTTGTGGAT GTAGACATAA TTGCTTCGCG ACCGTAACTG GGACTCACTA

3201 TTTTCTCTGG TCCCGCCGCA TCCATACCGC CAGTTGTTTA CCCTCACAAC GTTCCAGTAA CCGGGCATGT TCATCATCAG TAACCCGTAT CGTGAGCATC
     AAAAGAGACC AGGGCGGCGT AGGTATGGCG GTCAACAAAT GGGAGTGTTG CAAGGTCATT GGCCCGTACA AGTAGTAGTC ATTGGGCATA GCACTCGTAG

3301 CTCTCTCGTT TCATCGGTAT CATTACCCCC ATGAACAGAA ATTCCCCCTT ACACGGAGGC ATCAAGTGAC CAAACAGGAA AAAACCGCCC TTAACATGGC
     GAGAGAGCAA AGTAGCCATA GTAATGGGGG TACTTGTCTT TAAGGGGGAA TGTGCCTCCG TAGTTCACTG GTTTGTCCTT TTTTGGCGGG AATTGTACCG

3401 CCGCTTTATC AGAAGCCAGA CATTAACGCT TCTGGAGAAA CTCAACGAGC TGGACGCGGA TGAACAGGCA GACATCTGTG AATCGCTTCA CGACCACGCT
     GGCGAAATAG TCTTCGGTCT GTAATTGCGA AGACCTCTTT GAGTTGCTCG ACCTGCGCCT ACTTGTCCGT CTGTAGACAC TTAGCGAAGT GCTGGTGCGA

3501 GATGAGCTTT ACCGCAGGAT CCGGAAATTG TAAACGTTAA TATTTTGTTA AAATTCGCGT TAAATTTTTG TTAAATCAGC TCATTTTTTA ACCAATAGGC
     CTACTCGAAA TGGCGTCCTA GGCCTTTAAC ATTTGCAATT ATAAAACAAT TTTAAGCGCA ATTTAAAAAC AATTTAGTCG AGTAAAAAAT TGGTTATCCG

3601 CGAAATCGGC AAAATCCCTT ATAAATCAAA AGAATAGACC GAGATAGGGT TGAGTGTTGT TCCAGTTTGG AACAAGAGTC CACTATTAAA GAACGTGGAC
     GCTTTAGCCG TTTTAGGGAA TATTTAGTTT TCTTATCTGG CTCTATCCCA ACTCACAACA AGGTCAAACC TTGTTCTCAG GTGATAATTT CTTGCACCTG

3701 TCCAACGTCA AAGGGCGAAA AACCGTCTAT CAGGGCTATG GCCCACTACG TGAACCATCA CCCTAATCAA GTTTTTTGGG GTCGAGGTGC CGTAAAGCAC
     AGGTTGCAGT TTCCCGCTTT TTGGCAGATA GTCCCGATAC CGGGTGATGC ACTTGGTAGT GGGATTAGTT CAAAAAACCC CAGCTCCACG GCATTTCGTG

3801 TAAATCGGAA CCCTAAAGGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAAG CCGGCGAACG TGGCGAGAAA GGAAGGGAAG AAAGCGAAAG GAGCGGGCGC
     ATTTAGCCTT GGGATTTCCC TCGGGGGCTA AATCTCGAAC TGCCCCTTTC GGCCGCTTGC ACCGCTCTTT CCTTCCCTTC TTTCGCTTTC CTCGCCCGCG

3901 TAGGGCGCTG GCAAGTGTAG CGGTCACGCT GCGCGTAACC ACCACACCCG CCGCGCTTAA TGCGCCGCTA CAGGGCGCGT CCGGATCCTG CCTCGCGCGT
     ATCCCGCGAC CGTTCACATC GCCAGTGCGA CGCGCATTGG TGGTGTGGGC GGCGCGAATT ACGCGGCGAT GTCCCGCGCA GGCCTAGGAC GGAGCGCGCA

4001 TTCGGTGATG ACGGTGAAAA CCTCTGACAC ATGCAGCTCC CGGAGACGGT CACAGCTTGT CTGTAAGCGG ATGCCGGGAG CAGACAAGCC CGTCAGGGCG
     AAGCCACTAC TGCCACTTTT GGAGACTGTG TACGTCGAGG GCCTCTGCCA GTGTCGAACA GACATTCGCC TACGGCCCTC GTCTGTTCGG GCAGTCCCGC

4101 CGTCAGCGGG TGTTGGCGGG TGTCGGGGCG CAGCCATGAC CCAGTCACGT AGCGATAGCG GAGTGTATAC TGGCTTAACT ATGCGGCATC AGAGCAGATT
     GCAGTCGCCC ACAACCGCCC ACAGCCCCGC GTCGGTACTG GGTCAGTGCA TCGCTATCGC CTCACATATG ACCGAATTGA TACGCCGTAG TCTCGTCTAA
```

FIG._26E

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4201 GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATGCGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC
     CATGACTCTC ACGTGGTATA CGCCACACTT TATGGCGTGT CTACGCATTC CTCTTTTATG GCGTAGTCCG CGAGAAGGCG AAGGAGCGAG TGACTGAGCG

4301 TGCGCTCGGT CGTTCGGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG
     ACGCGAGCCA GCAAGCCGAC GCCGCTCGCC ATAGTCGAGT GAGTTTCCGC CATTATGCCA ATAGGTGTCT TAGTCCCCTA TTGCGTCCTT TCTTGTACAC

4401 AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC
     TCGTTTTCCG GTCGTTTTCC GGTCCTTGGC ATTTTTCCGG CGCAACGACC GCAAAAAGGT ATCCGAGGCG GGGGGACTGC TCGTAGTGTT TTTAGCTGCG

4501 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
     AGTTCAGTCT CCACCGCTTT GGGCTGTCCT GATATTTCTA TGGTCCGCAA AGGGGGACCT TCGAGGGAGC ACGCGAGAGG ACAAGGCTGG GACGGCGAAT

4601 CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT
     GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGCACCG CGAAAGAGTA TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA

4701 GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG
     CCCGACACAC GTGCTTGGGG GGCAAGTCGG GCTGGCGACG CGGAATAGGC CATTGATAGC AGAACTCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC

4801 GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGGACAG
     CGTCGTCGGT GACCATTGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG ATGTCTCAAG AACTTCACCA CCGGATTGAT GCCGATGTGA TCTTCCTGTC

4901 TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT
     ATAAACCATA GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTTCTCAA CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA

5001 TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT
     ACAAACGTTC GTCGTCTAAT GCGCGTCTTT TTTTCCTAGA GTTCTTCTAG GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA

5101 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA
     ATTCCCTAAA ACCAGTACTC TAATAGTTTT TCCTAGAAGT GGATCTAGGA AAATTTAATT TTTACTTCAA AATTTAGTTA GATTTCATAT ATACTCATTT

5201 CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT
     GAACCAGACT GTCAATGGTT ACGAATTAGT CACTCCGTGG ATAGAGTCGC TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGGC AGCACATCTA
```

FIG._ 26F

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5301 AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA
     TTGATGCTAT GCCCTCCCGA ATGGTAGACC GGGGTCACGA CGTTACTATG GCGCTCTGGG TGCGAGTGGC CGAGGTCTAA ATAGTCGTTA TTTGGTCGGT

5401 GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGCCAGTTA
     CGGCCTTCCC GGCTCGCGTC TTCACCAGGA CGTTGAAATA GGCGGAGGTA GGTCAGATAA TTAACAACGG CCCTTCGATC TCATTCATCA AGCGGTCAAT

5501 ATAGTTTGCG CAACGTTGTT GCCATTGCTG CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC GGTTCCCAAC GATCAAGGCG
     TATCAAACGC GTTGCAACAA CGGTAACGAC GTCCGTAGCA CCACAGTGCG AGCAGCAAAC CATACCGAAG TAAGTCGAGG CCAAGGGTTG CTAGTTCCGC

5601 AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT
     TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCAATCG AGGAAGCCAG GAGGCTAGCA ACAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA

5701 ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC
     TACCGTCGTG ACGTATTAAG AGAATGACAG TACGGTAGGC ATTCTACGAA AAGACACTGA CCACTCATGA GTTGGTTCAG TAAGACTCTT ATCACATACG

5801 GGCGACCGAG TTGCTCTTGC CCGGCGTCAA CACGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG
     CCGCTGGCTC AACGAGAACG GGCCGCAGTT GTGCCCTATT ATGGCGCGGT GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCCGC

5901 AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT
     TTTTGAGAGT TCCTAGAATG GCGACAACTC TAGGTCAAGC TACATTGGGT GAGCACGTGG GTTGACTAGA AGTCGTAGAA AATGAAAGTG GTCGCAAAGA

6001 GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTTGAATAC TCATACTCTT CCTTTTTCAA TATTATTGAA
     CCCACTCGTT TTTGTCCTTC CGTTTTACGG CGTTTTTTCC CTTATTCCCG CTGTGCCTTT ACAACTTATG AGTATGAGAA GGAAAAAGTT ATAATAACTT

6101 GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC
     CGTAAATAGT CCCAATAACA GAGTACTCGC CTATGTATAA ACTTACATAA ATCTTTTTAT TTGTTTATCC CCAAGGCGCG TGTAAAGGGG CTTTTCACGG

6201 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAATA GGCGTATCAC GAGGCCCTTT CGTCTTCAAT ACAGGTAGAC CTTTCGTAGA
     TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATTGG ATATTTTTAT CCGCATAGTG CTCCGGGAAA GCAGAAGTTA TGTCCATCTG GAAAGCATCT

6301 GATGTACAGT GAAATCCCCG AAATTATACA CATGACTGAA GGAAGGGAGC TCGTCATTCC CTGCCGGGTT ACGTCACCTA ACATCACTGT TACTTTAAAA
     CTACATGTCA CTTTAGGGGC TTTAATATGT GTACTGACTT CCTTCCCTCG AGCAGTAAGG GACGGCCCAA TGCAGTGGAT TGTAGTGACA ATGAAATTTT
```

FIG._ 26G

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6401 AAGTTTCCAC TTGACACTTT GATCCCTGAT GGAAAACGCA TAATCTGGGA CAGTAGAAAG GGCTTCATCA TATCAAATGC AACGTACAAA GAAATAGGGC
     TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCTTTTGCGT ATTAGACCCT GTCATCTTTC CCGAAGTAGT ATAGTTTACG TTGCATGTTT CTTTATCCCG

6501 TTCTGACCTG TGAAGCAACA GTCAATGGGC ATTTGTATAA GACAAACTAT CTCACACATC GACAAACCAA TACAATACAG GTAGACCTTT CGTAGAGATG
     AAGACTGGAC ACTTCGTTGT CAGTTACCCG TAAACATATT CTGTTTGATA GAGTGTGTAG CTGTTTGGTT ATGTTATGTC CATCTGGAAA GCATCTCTAC

6601 TACAGTGAAA TCCCCGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCCTGC CGGGTTACGT CACCTAACAT CACTGTTACT TTAAAAAAGT
     ATGTCACTTT AGGGGCTTTA ATATGTGTAC TGACTTCCTT CCCTCGAGCA GTAAGGGACG GCCCAATGCA GTGGATTGTA GTGACAATGA AATTTTTTCA

6701 TTCCACTTGA CACTTTGATC CCTGATGGAA AACGCATAAT CTGGGACAGT AGAAAGGGCT TCATCATATC AAATGCAACG TACAAAGAAA TAGGGCTTCT
     AAGGTGAACT GTGAAACTAG GGACTACCTT TTGCGTATTA GACCCTGTCA TCTTTCCCGA AGTAGTATAG TTTACGTTGC ATGTTTCTTT ATCCCGAAGA

6801 GACCTGTGAA GCAACAGTCA ATGGGCATTT GTATAAGACA AACTATCTCA CACATCGACA AACCAATACA ATCTACAGGT AGACCTTTCG TAGAGATGTA
     CTGGACACTT CGTTGTCAGT TACCCGTAAA CATATTCTGT TTGATAGAGT GTGTAGCTGT TTGGTTATGT TAGATGTCCA TCTGGAAAGC ATCTCTACAT

6901 CAGTGAAATC CCCGAAATTA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCCG GGTTACGTCA CCTAACATCA CTGTTACTTT AAAAAAGTTT
     GTCACTTTAG GGGCTTTAAT ATGTGTACTG ACTTCCTTCC CTCGAGCAGT AAGGGACGGC CCAATGCAGT GGATTGTAGT GACAATGAAA TTTTTTCAAA

7001 CCACTTGACA CTTTGATCCC TGATGGAAAA CGCATAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCAACGTA CAAAGAAATA GGGCTTCTGA
     GGTGAACTGT GAAACTAGGG ACTACCTTTT GCGTATTAGA CCCTGTCATC TTTCCCGAAG TAGTATAGTT TACGTTGCAT GTTTCTTTAT CCCGAAGACT

7101 CCTGTGAAGC AACAGTCAAT GGGCATTTGT ATAAGACAAA CTATCTCACA CATCGACAAA CCAATACAAT C
     GGACACTTCG TTGTCAGTTA CCCGTAAACA TATTCTGTTT GATAGAGTGT GTAGCTGTTT GGTTATGTTA G
```

FIG._24H

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  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG
  1 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N   A  Y  A  D   I  Q  M   T  Q  S   P  S  S  L
    ^met                                                                      ^start of light chain
    ^start of stII signal sequence

101 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC
    ACAGGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
 35  S  A  S   V  G  D   R  V  T  I   T  C  R   A  S  Q   D  V  S  T   A  V  A   W  Y  Q   Q  K  P  G   K  A  P
                                          ^CDR-L1

201 GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT
    CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA
 68 K  L  L   I  Y  S  A   S  F  L   Y  S  G   V  P  S  R   F  S  G   S  G  S   G  T  D  F   T  L  T   I  S  S
                   ^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAC ATTATACTAC TCCTCCCACG TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG
    GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101 L  Q  P  E   D  F  A   T  Y  Y   C  Q  Q  H   Y  T  T   P  P  T   F  G  Q  G   T  K  V   E  I  K   R  T  V  A
                                    ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
    GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135  A  P  S   V  F  I   F  P  P  S   D  E  Q   L  K  S   G  T  A  S   V  V  C   L  L  N   N  F  Y  P   R  E  A

501 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
    GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG
168 K  V  Q   W  K  V  D   N  A  L   Q  S  G   N  S  Q  E   S  V  T   E  Q  D   S  K  D  S   T  Y  S   L  S  S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA
    TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT
201 T  L  T  L   S  K  A   D  Y  E   K  H  K  V   Y  A  C   E  V  T   H  Q  G  L   S  S  P   V  T  K   S  F  N  R
```

FIG._27A

```
701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG
    CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC
235  G  E  C   G  A  S   S  G  M  A   D  P  N   R  F  R   G  K  D  L   A  O
                   ^end of light chain, start of gD tag

801 TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTAACTAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
    ACCGGGATCA TGCGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA
-23                                                               M  K  K  N  I   A  F  L  L   A  S  M   F  V  F
                                                                  ^start of stII

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG
    AGATAACGAT GTTTGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC
 -8 S  I  A  T   N  A  Y   A  E  V   Q  L  V  E   S  G  G   G  L  V   Q  P  G  G   S  L  R   L  S  C   A  A  S  G
                    ^start of heavy chain                                                                    ^CDR-H1

001 GCTTCACCAT TAGTGGTTCT TGGATACACT GGGTGCGTCA GGCCCCGGGT AAGGGCCTGG AATGGGTTGC TTGGATTGCT CCTTATAGCG GCGCTACTGA
    CGAAGTGGTA ATCACCAAGA ACCTATGTGA CCCACGCAGT CCGGGGCCCA TTCCCGGACC TTACCCAACG AACCTAACGA GGAATATCGC CGCGATGACT
 27  F  T  I   S  G  S   W  I  H  W   V  R  Q   A  P  G   K  G  L  E   W  V  A   W  I  A   P  Y  S  G   A  T  D
                                                                               ^CDR-H2

101 CTATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCGCGT CTGTGTAGGT TTTGTGTCG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
 60 Y  A  D   S  V  K  G   R  F  T   I  S  A   D  T  S  K   N  T  A   Y  L  Q   M  N  S  L   R  A  E   D  T  A

201 GTCTATTATT GTGCAAGAGA GGGGGGCTTG TACTGGGTGT TCGACTACTG GGGTCAAGGA ACACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT
    CAGATAATAA CACGTTCTCT CCCCCCGAAC ATGACCCACA AGCTGATGAC CCCAGTTCCT TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA
 93 V  Y  Y  C   A  R  E   G  G  L   Y  W  V  F   D  Y  W   G  Q  G   T  L  V  T   V  S  S   A  S  T   K  G  P  S
                    ^CDR-H3

301 CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC
    GCCAGAAGGG GGACCGTGGG AGGAGGTTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG
127  V  F  P   L  A  P   S  S  K  S   T  S  G   G  T  A   A  L  G  C   L  V  K   D  Y  F   P  E  P  V   T  V  S
```

FIG._27B

```
1401 GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC
     CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG
 160 W  N  S   G  A  L  T   S  G  V   H  T  F   P  A  V  L   Q  S  S   G  L  Y   S  L  S  S   V  V  T   V  P  S

1501 AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC
     TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC CAGCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTTGAG
 193 S  S  L  G   T  Q  T   Y  I  C   N  V  N  H   K  P  S   N  T  K   V  D  K  K   V  E  P   K  S  C   D  K  T  H

1601 ACCTCAGTGG CGGTGGCTCT GGTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGCGCT
     TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGCGAT TATTCCCCCG ATACTGGCTT TTACGGCTAC TTTTGCGCGA
 227  L  S  G   G  G  S   G  S  G  D   F  D  Y   E  K  M   A  N  A  N   K  G  A   M  T  E   N  A  D  E   N  A  L
      ^end of heavy chain
         ^start of gene III coat protein (267-end)

1701 ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT GGTGACGTTT CCGGCCTTGC TAATGGTAAT
     TGTCAGACTG CGATTTCCGT TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA
 260 Q  S  D   A  K  G  K   L  D  S   V  A  T   D  Y  G  A   A  I  D   G  F  I   G  D  V  S   G  L  A   N  G  N

1801 GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT TAATGAATAA TTTCCGTCAA TATTTACCTT
     CCACGATGAC CACTAAAACG ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA
 293 G  A  T  G   D  F  A   G  S  N   S  Q  M  A   Q  V  G   D  G  D   N  S  P  L   M  N  N   F  R  Q   Y  L  P  S

1901 CCCTCCCTCA ATCGGTTGAA TGTCGCCCTT TTGTCTTTAG CGCTGGTAAA CCATATGAAT TTTCTATTGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT
     GGGAGGGAGT TAGCCAACTT ACAGCGGGAA AACAGAAATC GCGACCATTT GGTATACTTA AAAGATAACT AACACTGTTT TATTTGAATA AGGCACCACA
 327  L  P  Q   S  V  E   C  R  P  F   V  F  S   A  G  K   P  Y  E  F   S  I  D   C  D  K   I  N  L  F   R  G  V

2001 CTTTGCGTTT CTTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT ACTGCGTAAT AAGGAGTCTT AA
     GAAACGCAAA GAAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCATTA TTCCTCAGAA TT
 360 F  A  F   L  L  Y  V   A  T  F   M  Y  V   F  S  T  F   A  N  I   L  R  N   K  E  S  O
```

FIG._27C

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG
  1 M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I  Q  M  T  Q  S  P  S  S  L
    ^met                                                                ^start of light chain
    ^start of stII signal sequence

101 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC
    ACAGGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
 35  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A  V  A  W  Y  Q  Q  K  P  G  K  A  P
                                          ^CDR-L1

201 GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTTCC GGGACGGATT TCACTCTGAC CATCAGCAGT
    CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA
 68 K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  S
                  ^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAC ATTATACTAC TCCTCCCACG TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG
    GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC
101 L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  H  Y  T  T  P  P  T  F  G  Q  G  T  K  V  E  I  K  R  T  V  A
                                    ^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
    GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L  N  N  F  Y  P  R  E  A

501 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
    GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA TTGAGGGTCC TCTCACAGTG TCTCGTCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTCG
168 K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T  Y  S  L  S  S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA
    TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT
201 T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R
```

FIG._28A

```
701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG
    CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC
235    G  E  C   G  A  S   S  G  M  A   D  P  N   R  F  R   G  K  D  L   A  O
                ^end of light chain, start of gD tag

801 TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTAACTAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
    ACCGGGATCA TGCGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA
-23                                                              M  K  N  I      A  F  L  L   A  S  M   F  V  F
                                                                ^start of stII

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG
    AGATAACGAT GTTTGCGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCAC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC
 -8 S  I  A  T   N  A  Y   A  E  V   Q  L  V   E  S  G  G   G  L  V   Q  P  G  G   S  L  R   L  S  C   A  A  S  G
                    ^start of heavy chain                                                                    ^CDR-H1

001 GCTTCACCAT TAGTAATTAT GGGATACACT GGGTGCGTCA GGCCCCGGGT AAGGGCCTGG AATGGGTTGG TAGGATTTCT CCTTCTAACG GCTCTACTTA
    CGAAGTGGTA ATCATTAATA CCCTATGTGA CCCACGCAGT CCGGGGCCCA TTCCCGGACC TTACCCAACC ATCCTAAAGA GGAAGATTGC CGAGATGAAT
 27   F  T  I   S  N  Y   G  I  H  W   V  R  Q   A  P  G   K  G  L  E   W  V  G   R  I  S   P  S  N  G   S  T  Y
                                                                                  ^CDR-H2

101 CTATGCCGAT AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCGCGT CTGTGTAGGT TTTTGTGTCG GATGGATGTT TACTTGTCGA ATTCTCGACT CCTGTGACGG
 60  Y  A  D   S  V  K  G   R  F  T   I  S  A   D  T  S  K   N  T  A   Y  L  Q   M  N  S  L   R  A  E   D  T  A

201 GTCTATTATT GTGCAAAATG CTCGGTCAGG TTCGCTTACT GGGGTCAAGG AACACTAGTC ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC
    CAGATAATAA CACGTTTTAC GAGCCAGTCC AAGCGAATGA CCCCAGTTCC TTGTGATCAG TGGCAGAGGA GCCGGAGGTG GTTCCCGGGT AGCCAGAAGG
 93 V  Y  Y  C   A  K  C   S  V  R   F  A  Y  W   G  Q  G   T  L  V   T  V  S  S   A  S  T   K  G  P   S  V  F  P
                       ^CDR-H3
```

FIG._ 28B

```
01 CCCTGGCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC
   GGGACCGTGG GAGGAGGTTC TCGTGGAGAC CCCCGTGTCG CCGGGACCCG ACGGACCAGT TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG
27  L  A  P   S  S  K   S  T  S  G   G  T  A   A  L  G   C  L  V  K   D  Y  F   P  E  P   V  T  V  S   W  N  S

01 AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG
   TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCACT GGCACGGGAG GTCGTCGAAC
60  G  A  L   T  S  G  V   H  T  F   P  A  V   L  Q  S  S   G  L  Y   S  L  S   S  V  V  T   V  P  S   S  S  L

01 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTCGACAAG AAAGTTGAGC CCAAATCTTG TGACAAAACT CACCTCAGTG
   CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGGT CGTTGTGGTT CCAGCTGTTC TTTCAACTCG GGTTTAGAAC ACTGTTTTGA GTGGAGTCAC
93 G  T  Q  T   Y  I  C   N  V  N   H  K  P  S   N  T  K   V  D  K   K  V  E  P   K  S  C   D  K  T   H  L  S  G
                                                                                                    ^end of heavy chain
                                                        start of gene III coat protein (267-end)^

01 GCGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT GAAAACGCGC TACAGTCTGA
   CGCCACCGAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA CCGTTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA CTTTTGCGCG ATGTCAGACT
7   G  G  S   G  S  G   D  F  D  Y   E  K  M   A  N  A   N  K  G  A   M  T  E   N  A  D   E  N  A  L   Q  S  D

01 CGCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT
   GCGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC GATTACCATT ACCACGATGA
60 A  K  G   K  L  D  S   V  A  T   D  Y  G   A  A  I  D   G  F  I   G  D  V   S  G  L  A   N  G  N   G  A  T

01 GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTTACCT TCCCTCCCTC
   CCACTAAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGGA AATTACTTAT TAAAGGCAGT TATAAATGGA AGGGAGGGAG
93 G  D  F  A   G  S  N   S  Q  M   A  Q  V  G   D  G  D   N  S  P   L  M  N  N   F  R  Q   Y  L  P   S  L  P  Q

01 AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT
   TTAGCCAACT TACAGCGGGA AAACAGAAAT CGCGACCATT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAAT AAGGCACCAC AGAAACGCAA
27  S  V  E   C  R  P   F  V  F  S   A  G  K   P  Y  E   F  S  I  D   C  D  K   I  N  L   F  R  G  V   F  A  F

01 TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAA
   AGAAAATATA CAACGGTGGA AATACATACA TAAAAGATGC AAACGATTGT ATGACGCATT ATTCCTCAGA ATT
60 L  L  Y   V  A  T  F   M  Y  V   F  S  T   F  A  N  I   L  R  N   K  E  S   O
```

FIG._ 28C

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
  1 M  K  K  N   I  A  F  L  L  A   S  M  F  V   F  S  I   A  T  N   A  Y  A  S   D  I  Q   M  T  Q   S  P  S  S
    ^met
    ^start of stII signal sequence                                             ^light chain start

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
    GGGACAGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
 35  L  S  A   S  V  G   D  R  V  T   I  T  C   R  A  S   Q  D  V  S   T  A  V   A  W  Y   Q  Q  K  P   G  K  A
                                                ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
    AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
 68 P  K  L   L  I  Y  S   A  S  F   L  Y  S   G  V  P  S   R  F  S   G  S  G   S  G  T  D   F  T  L   T  I  S
                       ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAGC AATCTTATAC TACTCCTCCC ACGTTCGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG
    TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S  L  Q  P   E  D  F   A  T  Y   Y  C  Q  Q   S  Y  T   T  P  P   T  F  G  Q   G  T  K   V  E  I   K  R  T  V
                                           ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
    ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135  A  A  P   S  V  F   I  F  P  P   S  D  E   Q  L  K   S  G  T  A   S  V  V   C  L  L   N  N  F  Y   P  R  E

501 GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
    CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG
168 A  K  V   Q  W  K  V   D  N  A   L  Q  S   G  N  S  Q   E  S  V   T  E  Q   D  S  K  D   S  T  Y   S  L  S

601 AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
    TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S  T  L  T   L  S  K   A  D  Y   E  K  H  K   V  Y  A   C  E  V   T  H  Q  G   L  S  S   P  V  T   K  S  F  N
```

FIG._ 29A

```
 1 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
   TGTCCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT
35   R  G  E   C  G  A   S  S  G  M   A  D  P   N  R  F   R  G  K  D   L  A  O
                  ^end of light chain, start of gD tag

 1 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT
   AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
 3                                                                M  K  K   N   I  A  F  L   L  A  S   M  F  V
                                                                  ^start of stII

 1 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
   AAAAGATAAC GATGTTTGCG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA
 9 F  S  I  A   T  N  A   Y  A  E   V  Q  L  V   E  S  G   G  G  L   V  Q  P  G   G  S  L   R  L  S   C  A  A  S
                      ^start of heavy chain                                                                         ^CDR-H1

 1 CTGGCTTCAC CATTAGTGGT TCTGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGGTAGGATT TCTCCTTATG GCGGCAATAC
   GACCGAAGTG GTAATCACCA AGACTATATG TGACCCACGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCATCCTAA AGAGGAATAC CGCCGTTATG
 6   G  F  T   I  S  G   S  D  I  H   W  V  R   Q  A  P   G  K  G  L   E  W  V   G  R  I   S  P  Y  G   G  N  T
                                                                                    ^CDR-H2

 1 TAACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
   ATTGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTCG CGTCTGTGTA GGTTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
 9  N  Y  A   D  S  V  K   G  R  F   T  I  S   A  D  T  S   K  N  T   A  Y  L   Q  M  N  S   L  R  A   E  D  T

 1 GCCGTCTATT ATTGTGCAAG AGTCGGCGGC CTCAAGTTGC TGTTCGACTA CTGGGGTCAA GGAACACTAG TCACCGTCTC CTCGGCCTCC ACCAAGGGCC
   CGGCAGATAA TAACACGTTC TCAGCCGCCG GAGTTCAACG ACAAGCTGAT GACCCCAGTT CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG
 2 A  V  Y  Y   C  A  R   V  G  G   L  K  L  L   F  D  Y   W  G  Q   G  T  L  V   T  V  S   S  A  S   T  K  G  P
                          ^CDR-H3

 1 CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT
   GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA GTTCCTGATG AAGGGGCTTG GCCACTGCCA
 6   S  V  F   P  L  A   P  S  S  K   S  T  S   G  G  T   A  A  L  G   C  L  V   K  D  Y   F  P  E  P   V  T  V
```

FIG._ 29B

```
1401 GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC
     CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACCA CTGGCACGGG
 159  S  W  N   S  G  A  L   T  S  G   V  H  T   F  P  A  V   L  Q  S   S  G  L   Y  S  L  S   S  V  V   T  V  P

1501 TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTCGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA
     AGGTCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG TTCCAGCTGT TCTTTCAACT CGGGTTTAGA ACACTGTTTT
 192 S  S  S  L   G  T  Q   T  Y  I   C  N  V  N   H  K  P   S  N  T   K  V  D  K   K  V  E   P  K  S   C  D  K  T

1601 CTCACGGCCG CATGAAACAG CTAGAGGACA AGGTCGAAGA GCTACTCTCC AAGAACTACC ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTCGG
     GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGATGG TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC
 226  H  G  R   M  K  Q   L  E  D  K   V  E  E   L  L  S   K  N  Y  H   L  E  N   E  V  A   R  L  K  K   L  V  G
        ^end of heavy chain, start of leucine zipper

1701 GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT
     CCTCGCGCCT TTCGAATCAC CGCCACCGAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA CCGTTTGCGA TTATTCCCCC GATACTGGCT TTTACGGCTA
 259  E  R  G   K  L  S  G   G  G  S   G  S  G   D  F  D  Y   E  K  M   A  N  A   N  K  G  A   M  T  E   N  A  D
                  ^end of leucine zipper, gene III coat protein (267-end)

1801 GAAAACGCGC TACAGTCTGA CGCTAAAGGC AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCTTG
     CTTTTGCGCG ATGTCAGACT GCGATTTCCG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA ACCACTGCAA AGGCCGGAAC
 292 E  N  A  L   Q  S  D   A  K  G   K  L  D  S   V  A  T   D  Y  G   A  A  I  D   G  F  I   G  D  V   S  G  L  A

1901 CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA
     GATTACCATT ACCACGATGA CCACTAAAAC GACCGAGATT AAGGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGGA AATTACTTAT TAAAGGCAGT
 326  N  G  N   G  A  T   G  D  F  A   G  S  N   S  Q  M   A  Q  V  G   D  G  D   N  S  P   L  M  N  N   F  R  Q

2001 ATATTTACCT TCCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA
     TATAAATGGA AGGGAGGGAG TTAGCCAACT TACAGCGGGA AAACAGAAAT CGCGACCATT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTTGAAT
 359  Y  L  P   S  L  P  Q   S  V  E   C  R  P   F  V  F  S   A  G  K   P  Y  E   F  S  I  D   C  D  K   I  N  L

2101 TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAA
     AAGGCACCAC AGAAACGCAA AGAAAATATA CAACGGTGGA AATACATACA TAAAAGATGC AAACGATTGT ATGACGCATT ATTCCTCAGA ATT
 392 F  R  G  V   F  A  F   L  L  Y   V  A  T  F   M  Y  V   F  S  T   F  A  N  I   L  R  N   K  E  S   O
```

FIG._29C

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
  1 M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  S  D  I  Q  M  T  Q  S  P  S  S
    ^start of stII signal sequence                                           ^light chain start
    ^met

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
    GGGACAGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
 35  L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  S  T  A  V  A  W  Y  Q  Q  K  P  G  K  A
                                              ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
    AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
 68 P  K  L  L  I  Y  S  A  S  F  L  Y  S  G  V  P  S  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S
                       ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAGC AATCTTATAC TACTCCTCCC ACGTTCGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG
    TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  S  Y  T  T  P  P  T  F  G  Q  G  T  K  V  E  I  K  R  T  V
                                         ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
    ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L  N  N  F  Y  P  R  E

501 GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
    CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG
168 A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T  Y  S  L  S

601 AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
    TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N
```

FIG._30A

```
701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
    TGTCCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT
35   R  G  E   C  G  A   S  S  G  M   A  D  P   N  R  F   R  G  K  D   L  A  O
                   ^end of light chain, start of gD tag

01  TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT
    AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
23
                                                               M  K  K  N   I  A  F  L   L  A  S   M  F  V
                                                               ^start of stII

01  TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
    AAAAGATAAC GATGTTTGCG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA
-9  F  S  I  A   T  N  A   Y  A  E   V  Q  L  V   E  S  G   G  G  L   V  Q  P  G   G  S  L   R  L  S   C  A  A  S
                     ^start of heavy chain                                                                  ^CDR-H1

01  CTGGCTTCAC CATTACTAAT TCCGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGCTACTATT TATCCTTATG GCGGCTATAC
    GACCGAAGTG GTAATGATTA AGGCTATATG TGACCCACGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACGATGATAA ATAGGAATAC CGCCGATATG
6    G  F  T   I  T  N   S  D  I  H   W  V  R   Q  A  P   G  K  G  L   E  W  V   A  T  I   Y  P  Y  G   G  Y  T
                                                                                 ^CDR-H2

1   TTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
    AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTCG CGTCTGTGTA GGTTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
9   Y  Y  A   D  S  V  K   G  R  F   T  I  S   A  D  T  S   K  N  T   A  Y  L   Q  M  N  S   L  R  A   E  D  T

1   GCCGTCTATT ATTGTGCAAG AGGGGGCGGG ATGGACGGCT ACGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG
    CGGCAGATAA TAACACGTTC TCCCCCGCCC TACCTGCCGA TGCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGGTTCC
2   A  V  Y  Y   C  A  R   G  G  G   M  D  G  Y   V  M  D   Y  W  G   Q  G  T  L   V  T  V   S  S  A   S  T  K  G
                           ^CDR-H3

1   GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
    CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCGTG GAGACCCCCG TGTCGCCGGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG
6    P  S  V   F  P  L   A  P  S  S   K  S  T   S  G  G   T  A  A  L   G  C  L   V  K  D   Y  F  P  E   P  V  T
```

FIG._30B

```
1401 GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG
     CCACAGCACC TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGGAAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC
 159 V  S  W   N  S  G   A  L  T  S   G  V  H   T  F  P  A   V  L  Q   S  S  G   L  Y  S  L   S  S  V   V  T  V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA
     GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGTT CGGGTCGTTG TGGTTCCAGC TGTTCTTTCA ACTCGGGTTT AGAACACTGT
 192 P  S  S  S   L  G  T   Q  T  Y   I  C  N  V   N  H  K   P  S  N   T  K  V  D   K  K  V   E  P  K   S  C  D  K

1601 AAACTCACGG CCGCATGAAA CAGCTAGAGG ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT
     TTTGAGTGCC GGCGTACTTT GTCGATCTCC TGTTCCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTTGAACA
 226  T  H  G   R  M  K   Q  L  E  D   K  V  E   E  L  L   S  K  N  Y   H  L  E   N  E  V   A  R  L  K   K  L  V
           ^end of heavy chain, start of leucine zipper

1701 CGGGGAGCGC GGAAAGCTTA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCC
     GCCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACTAAAAC TAATACTTTT CTACCGTTTG CGATTATTCC CCCGATACTG GCTTTTACGG
 259 G  E  R   G  K  L  S   G  G  G   S  G  S   G  D  F  D   Y  E  K   M  A  N   A  N  K  G   A  M  T   E  N  A
                       ^end of leucine zipper,  start of gene III coat protein (267-end)

.801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTGGTGAC GTTTCCGGCC
     CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAAGGCCGG
 292 D  E  N  A   L  Q  S   D  A  K   G  K  L  D   S  V  A   T  D  Y   G  A  A  I   D  G  F   I  G  D   V  S  G  L

1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTTAATGA ATAATTTCCG
     AACGATTACC ATTACCACGA TGACCACTAA AACGACCGAG ATTAAGGGTT TACCGAGTTC AGCCACTGCC ACTATTAAGT GGAAATTACT TATTAAAGGC
 326  A  N  G   N  G  A   T  G  D  F   A  G  S   N  S  Q   M  A  Q  V   G  D  G   D  N  S   P  L  M  N   N  F  R

2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC
     AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAAAACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTTG
 359 Q  Y  L   P  S  L  P   Q  S  V   E  C  R   P  F  V  F   S  A  G   K  P  Y   E  F  S  I   D  C  D   K  I  N

2101 TTATTCCGTG GTGTCTTTGC GTTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA ACATACTGCG TAATAAGGAG TCTTAA
     AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAAATACAT ACATAAAAGA TGCAAACGAT TGTATGACGC ATTATTCCTC AGAATT
 392 L  F  R  G   V  F  A   F  L  L   Y  V  A  T   F  M  Y   V  F  S   T  F  A  N   I  L  R   N  K  E   S  O
```

FIG._30C

```
  1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
    TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
  1 M  K  K  N   I  A  F   L  L  A   S  M  F  V   F  S  I   A  T  N   A  Y  A  S   D  I  Q   M  T  Q   S  P  S  S
    ^met                                                                          ^light chain start

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
    GGGACAGGCG GAGACACCCG CTATCCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCCTTTTCG
 35  L  S  A   S  V  G   D  R  V  T   I  T  C   R  A  S   Q  D  V  S   T  A  V   A  W  Y   Q  Q  K  P   G  K  A
                                               ^CDR-L1

201 TCCGAAGCTT CTGATTTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTCGCTTCTC TGGTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
    AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
 68 P  K  L   L  I  Y  S   A  S  F   L  Y  S   G  V  P  S   R  F  S   G  S  G   S  G  T  D   F  T  L   T  I  S
                      ^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTCAGC AATCTTATAC TACTCCTCCC ACGTTCGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG
    TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S  L  Q  P   E  D  F   A  T  Y   Y  C  Q  Q   S  Y  T   T  P  P   T  F  G  Q   G  T  K   V  E  I   K  R  T  V
                                           ^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
    ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135  A  A  P   S  V  F   I  F  P  P   S  D  E   Q  L  K   S  G  T  A   S  V  V   C  L  L   N  N  F  Y   P  R  E

501 GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
    CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGTCTCGTC CTGTCGTTCC TGTCGTGGAT GTCGGAGTCG
168  A  K  V   Q  W  K  V   D  N  A   L  Q  S   G  N  S  Q   E  S  V   T  E  Q   D  S  K  D   S  T  Y   S  L  S

601 AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
    TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S  T  L  T   L  S  K   A  D  Y   E  K  H  K   V  Y  A   C  E  V   T  H  Q  G   L  S  S   P  V  T   K  S  F  N
```

FIG._31A

```
1 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
  TGTCCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CGGCCTGCGT
5  R  G  E   C  G  A   S  S  G  M   A  D  P   N  R  F   R  G  K  D   L  A  O
                   ^end of light chain, start of gD tag

1 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTC TTCTTGCATC TATGTTCGTT
  AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTGA TCTCCAACTC CACTAAAATA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
3                                                                  M  K  K  N   I  A  F  L   L  A  S   M  F  V
                                                                   ^start of stII

1 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
  AAAAGATAAC GATGTTTGCG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGGTC CCCCGAGTGA GGCAAACAGG ACACGTCGAA
9 F  S  I  A   T  N  A   Y  A  E   V  Q  L  V   E  S  G   G  G  L   V  Q  P  G   G  S  L   R  L  S   C  A  A  S
                    ^start of heavy chain                                                                       ^CDR-H1

1 CTGGCTTCAC CATTAATAAT TATGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAGGGCC TGGAATGGGT TGGTTATATT TCTCCTCCTA GCGGCGCTAC
  GACCGAAGTG GTAATTATTA ATACTATATG TGACCCACGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGCGATG
5  G  F  T   I  N  N   Y  D  I  H   W  V  R   Q  A  P   G  K  G  L   E  W  V   G  Y  I   S  P  P  S   G  A  T
                                                                              ^CDR-H2

1 TTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
  AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTCG CGTCTGTGTA GGTTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
9 Y  Y  A   D  S  V  K   G  R  F   T  I  S   A  D  T  S   K  N  T   A  Y  L   Q  M  N  S   L  R  A   E  D  T

1 GCCGTCTATT ATTGTGCAAG AATGGTCGGC ATGCGGAGGG GGGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCCTCGGCC TCCACCAAGG
  CGGCAGATAA TAACACGTTC TTACCAGCCG TACGCCTCCC CCCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGGTTCC
2 A  V  Y  Y   C  A  R   M  V  G   M  R  R  G   V  M  D   Y  W  G   Q  G  T  L   V  T  V   S  S  A   S  T  K  G
                         ^CDR-H3

1 GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
  CGGGTAGCCA GAAGGGGGAC CGTGGGAGGA GGTTCTCGTG GAGACCCCCG TGTCGCCGGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG
6  P  S  V   F  P  L   A  P  S  S   K  S  T   S  G  G   T  A  A  L   G  C  L   V  K  D   Y  F  P  E   P  V  T
```

FIG._31B

```
1401 GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG
     CCACAGCACC TTGAGTCCGC GGGACTGGTC GCCGCACGTG TGGAAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGGG AGTCGTCGCA CCACTGGCAC
 159 V  S  W   N  S  G  A   L  T  S   G  V  H   T  F  P  A   V  L  Q   S  S  G   L  Y  S  L   S  S  V   V  T  V

1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCAAA TCTTGTGACA
     GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTGC ACTTAGTGTT CGGGTCGTTG TGGTTCCAGC TGTTCTTTCA ACTCGGGTTT AGAACACTGT
 192 P  S  S  S   L  G  T   Q  T  Y   I  C  N  V   N  H  K   P  S  N   T  K  V  D   K  K  V   E  P  K   S  C  D  K

1601 AAACTCACGG CCGCATGAAA CAGCTAGAGG ACAAGGTCGA AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAACTTGT
     TTTGAGTGCC GGCGTACTTT GTCGATCTCC TGTTCCAGCT TCTCGATGAG AGGTTCTTGA TGGTGGATCT CTTACTTCAC CGTTCTGAGT TTTTTGAACA
 226  T  H  G   R  M  K   Q  L  E  D   K  V  E   E  L  L   S  K  N  Y   H  L  E   N  E  V   A  R  L  K   K  L  V
            ^end of heavy chain, start of leucine zipper

1701 CGGGGAGCGC GGAAAGCTTA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCC
     GCCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACTAAAAC TAATACTTTT CTACCGTTTG CGATTATTCC CCCGATACTG GCTTTTACGG
 259  G  E  R   G  K  L  S   G  G  G   S  G  S   G  D  F  D   Y  E  K   M  A  N   A  N  K  G   A  M  T   E  N  A
              ^end of leucine zipper
                 ^gene III coat protein (267-end)

1801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA TCGATGGTTT CATTGGTGAC GTTTCCGGCC
     CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAAGGCCGG
 292 D  E  N  A   L  Q  S   D  A  K   G  K  L  D   S  V  A   T  D  Y   G  A  A  I   D  G  F   I  G  D   V  S  G  L

1901 TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTTAATGA ATAATTTCCG
     AACGATTACC ATTACCACGA TGACCACTAA AACGACCGAG ATTAAGGGTT TACCGAGTTC AGCCACTGCC ACTATTAAGT GGAAATTACT TATTAAAGGC
 326  A  N  G   N  G  A   T  G  D  F   A  G  S   N  S  Q   M  A  Q  V   G  D  G   D  N  S   P  L  M  N   N  F  R

2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC CCTTTTGTCT TTAGCGCTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC
     AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAAAACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTTG
 359 Q  Y  L   P  S  L  P   Q  S  V   E  C  R   P  F  V  F   S  A  G   K  P  Y   E  F  S  I   D  C  D   K  I  N

2101 TTATTCCGTG GTGTCTTTGC GTTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA ACATACTGCG TAATAAGGAG TCTTAA
     AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAAATACAT ACATAAAAGA TGCAAACGAT TGTATGACGC ATTATTCCTC AGAATT
 392 L  F  R  G   V  F  A   F  L  L   Y  V  A  T   F  M  Y   V  F  S   T  F  A  N   I  L  R   N  K  E   S  O
```

FIG._31C

```
  1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
    CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATGTA GAGGTTGAGG TGATTTTATG AAAAAGAATA TCGCATTTCT TCTTGCATCT ATGTTCGTTT TTTCTATTGC TACAAATGCC
    AGTGCATTTT TCCCATACAT CTCCAACTCC ACTAAAATAC TTTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
  0                                         M   K  K  N  I   A  F  L   L  A  S   M  F  V  F   S  I  A   T  N  A
                                            ^start of stII signal sequence

501 TATGCAGATA TCCAGATGAC CCAGTCCCCG AGCTCCCTGT CCGCCTCTGT GGGCGATAGG GTCACCATCA CCTGCCGTGC CAGTCAGGAT GTGTCCACTG
    ATACGTCTAT AGGTCTACTG GGTCAGGGGC TCGAGGGACA GGCGGAGACA CCCGCTATCC CAGTGGTAGT GGACGGCACG GTCAGTCCTA CACAGGTGAC
 21 Y  A  D  I   Q  M  T   Q  S  P   S  S  L  S   A  S  V   G  D  R   V  T  I  T   C  R  A   S  Q  D   V  S  T  A
          ^start of light chain                                                       ^CDR-L1
            ^EcoRV

601 CTGTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCCTCTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
    GACATCGGAC CATAGTTGTC TTTGGTCCTT TTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
 55   V  A  W   Y  Q  Q   K  P  G  K   A  P  K   L  L  I   Y  S  A  S   F  L  Y   S  G  V   P  S  R  F   S  G  S
                                                              ^CDR-L2

701 CGGTTCCGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTC
    GCCAAGGCCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGGTGCAAG
 88  G  S  G   T  D  F  T   L  T  I   S  S  L   Q  P  E  D   F  A  T   Y  Y  C   Q  Q  S  Y   T  T  P   P  T  F
                                                                                 ^CDR-L3
```

FIG._32A

```
1 GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
  CCTGTCCCAT GGTTCCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GGCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
1 G Q G T  K V E  I K R  T V A A  P S V  F I F  P P S D  E Q L  K S G  T A S V
       ^KpnI

1 TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA
  AACACACGGA CGACTTATTG AAGATAGGGT CTCTCCGGTT TCATGTCACC TTCCACCTAT TGCGGGAGGT TAGCCCATTG AGGGTCCTCT CACAGTGTCT
5  V C L  L N N  F Y P R  E A K  V Q W  K V D N  A L Q  S G N  S Q E S  V T E

1 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA AGTCACCCAT
  CGTCCTGTCG TTCCTGTCGT GGATGTCGGA GTCGTCGTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TGCGGACGCT TCAGTGGGTA
8 Q D S  K D S T  Y S L  S S T  L T L S  K A D  Y E K  H K V Y  A C E  V T H

1 CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGCGGT AAGGACCTGG
  GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGGTCGAGG CCATACCGAC TAGGCTTGGC AAAGGCGCCA TTCCTGGACC
  Q G L S  S P V  T K S  F N R G  E C G  A S S  G M A D  P N R  F R G  K D L A
                                                     ^end of light chain, start of gD tag

1 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTACG CAAGTTCACG TAAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
  GTATTGAGCT CCGACTAGGA GATGCGGCCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCCA TTGATCTCCA ACTCCACTAA AATACTTTTT
5  O
3
                                                                                                     M  K  K
                                                                                                     ^start of stII

1 GAATATCGCA TTTCTTCTTG CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGCGTACGC TGAGGTTCAG CTGGTGGAGT CTGGCGGTGG CCTGGTGCAG
  CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACGTC
) N I A  F L L A  S M F  V F S  I A T N  A Y A  E V Q  L V E S  G G G  L V Q
                                                          ^start of heavy chain
                                                               ^BsiWi
```

FIG._32B

```
1401 CCAGGGGGCT CACTCCGTTT GTCCTGTGCA GCTTCTGGCT TCACCATTAG TGGTTCTTGG ATACACTGGG TGCGTCAGGC CCCGGGTAAG GGCCTGGAAT
     GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTGGTAATC ACCAAGAACC TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
  14 P  G  G  S   L  R  L   S  C  A   A  S  G  F   T  I  S   G  S  W   I  H  W  V   R  Q  A   P  G  K   G  L  E  W
                                      ^CDR-H1

1501 GGGTTGCTTG GATTGCTCCT TATAGCGGCG CTACTGACTA TGCCGATAGC GTCAAGGGCC GTTTCACTAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA
     CCCAACGAAC CTAACGAGGA ATATCGCCGC GATGACTGAT ACGGCTATCG CAGTTCCCGG CAAAGTGATA TTCGCGTCTG TGTAGGTTTT TGTGTCGGAT
  48   V  A  W   I  A  P   Y  S  G  A   T  D  Y   A  D  S   V  K  G  R   F  T  I   S  A  D   T  S  K  N   T  A  Y
           ^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTG CAAGAGAGGG GGGCTTGTAC TGGGTGTTCG ACTACTGGGG TCAAGGAACA
     GGATGTTTAC TTGTCGAATT CTCGACTCCT GTGACGGCAG ATAATAACAC GTTCTCTCCC CCCGAACATG ACCCACAAGC TGATGACCCC AGTTCCTTGT
  81 L  Q  M   N  S  L  R   A  E  D   T  A  V   Y  Y  C  A   R  E  G   G  L  Y   W  V  F  D   Y  W  G   Q  G  T
                                                                ^CDR-H3

1701 CTAGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC
     GATCAGTGGC AGAGGAGCCG GAGGTGGTTC CCGGGTAGCC AGAAGGGGGA CCGTGGGAGG AGGTTCTCGT GGAGACCCCC GTGTCGCCGG GACCCGACGG
 114 L  V  T  V   S  S  A   S  T  K   G  P  S  V   F  P  L   A  P  S   S  K  S  T   S  G  G   T  A  A   L  G  C  L
                                     ^ApaI

1801 TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC AGTCCTCAGG
     ACCAGTTCCT GATGAAGGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGGACTGGT CGCCGCACGT GTGGAAGGGC CGACAGGATG TCAGGAGTCC
 148   V  K  D   Y  F  P   E  P  V  T   V  S  W   N  S  G   A  L  T  S   G  V  H   T  F  P   A  V  L  Q   S  S  G

1901 ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTC
     TGAGATGAGG GAGTCGTCGC ACCACTGGCA CGGGAGGTCG TCGAACCCGT GGGTCTGGAT GTAGACGTTG CACTTAGTGT TCGGGTCGTT GTGGTTCCAG
 181   L  Y  S   L  S  S  V   V  T  V   P  S  S   S  L  G  T   Q  T  Y   I  C  N   V  N  H  K   P  S  N   T  K  V

2001 GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGGTGGCTCT GGTTCCGGTG ATGCTCGGTT GCCGCCGGGC GTTTTTTATG
     CTGTTCTTTC AACTCGGGTT TAGAACACTG TTTTGAGTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TACGAGCCAA CGGCGGCCCG CAAAAAATAC
 214 D  K  K  V   E  P  K   S  C  D   K  T  H  L   O

2101 CTAGCGCCGC CCTATACCTT GTCTGCCTCC CCGCGTTGCG TCGCGGTGCA TGGAGCCGGG CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGCTAAC
     GATCGCGGCG GGATATGGAA CAGACGGAGG GGCGCAACGC AGCGCCACGT ACCTCGGCCC GGTGGAGCTG GACTTACCTT CGGCCGCCGT GGAGCGATTG
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FIG._32C

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2201 GGATTCACCA CTCCAAGAAT TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGCGCAA ACCAACCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT
     CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAACG CCTCTTGACA CTTACGCGTT TGGTTGGGAA CCGTCTTGTA TAGGTAGCGC AGGCGGTAGA

2301 CCAGCAGCCG CACGCGGCGC ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCGCATGA TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGGG
     GGTCGTCGGC GTGCGCCGCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACGCGTACT AGCACGAGGA CAGCAACTCC TGGGCCGATC CGACCGCCCC

2401 TTGCCTTACT GGTTAGCAGA ATGAATCACC GATACGCGAG CGAACGTGAA GCGACTGCTG CTGCAAAACG TCTGCGACCT GAGCAACAAC ATGAATGGTC
     AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC GACGTTTTGC AGACGCTGGA CTCGTTGTTG TACTTACCAG

2501 TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATTATG TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCTGTG
     AAGCCAAAGG CACAAAGCAT TTCAGACCTT TGCGCCTTCA GTCGCGGGAC GTGGTAATAC AAGGCCTAGA CGTAGCGTCC TACGACGACC GATGGGACAC

2601 GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATT TTTCTCTGGT CCCGCCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG
     CTTGTGGATG TAGACATAAT TGCTTCGCGA CCGTAACTGG GACTCACTAA AAAGAGACCA GGGCGGCGTA GGTATGGCGG TCAACAAATG GGAGTGTTGC

2701 TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCTCTCGTTT CATCGGTATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA
     AAGGTCATTG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA GTAGCCATAG TAATGGGGGT ACTTGTCTTT AAGGGGGAAT

2801 CACGGAGGCA TCAAGTGACC AAACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT
     GTGCCTCCGT AGTTCACTGG TTTGTCCTTT TTTGGCGGGA ATTGTACCGG GCGAAATAGT CTTCGGTCTG TAATTGCGAA GACCTCTTTG AGTTGCTCGA

2901 GGACGCGGAT GAACAGGCAG ACATCTGTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA CCGCAGGATC CGGAAATTGT AAACGTTAAT ATTTTGTTAA
     CCTGCGCCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGCGAC TACTCGAAAT GGCGTCCTAG GCCTTTAACA TTTGCAATTA TAAAACAATT

3001 AATTCGCGTT AAATTTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT
     TTAAGCGCAA TTTAAAAACA ATTTAGTCGA GTAAAAAATT GGTTATCCGG CTTTAGCCGT TTTAGGGAAT ATTTAGTTTT CTTATCTGGC TCTATCCCAA

3101 GAGTGTTGTT CCAGTTTGGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA AGGGCGAAAA ACCGTCTATC AGGGCTATGG CCCACTACGT
     CTCACAACAA GGTCAAACCT TGTTCTCAGG TGATAATTTC TTGCACCTGA GGTTGCAGTT TCCCGCTTTT TGGCAGATAG TCCCGATACC GGGTGATGCA
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FIG._ 32D

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3201 GAACCATCAC CCTAATCAAG TTTTTTGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC CCTAAAGGGA GCCCCCGATT TAGAGCTTGA CGGGGAAAGC
     CTTGGTAGTG GGATTAGTTC AAAAAACCCC AGCTCCACGG CATTTCGTGA TTTAGCCTTG GGATTTCCCT CGGGGGCTAA ATCTCGAACT GCCCCTTTCG

3301 CGGCGAACGT GGCGAGAAAG GAAGGGAAGA AAGCGAAAGG AGCGGGCGCT AGGGCGCTGG CAAGTGTAGC GGTCACGCTG CGCGTAACCA CCACACCCGC
     GCCGCTTGCA CCGCTCTTTC CTTCCCTTCT TTCGCTTTCC TCGCCCGCGA TCCCGCGACC GTTCACATCG CCAGTGCGAC GCGCATTGGT GGTGTGGGCG

3401 CGCGCTTAAT GCGCCGCTAC AGGGCGCGTC CGGATCCTGC CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGTC
     GCGCGAATTA CGCGGCGATG TCCCGCGCAG GCCTAGGACG GAGCGCGCAA AGCCACTACT GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG

3501 ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA
     TGTCGAACAG ACATTCGCCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGCG CAGTCGCCCA CAACCGCCCA CAGCCCCGCG TCGGTACTGG GTCAGTGCAT

3601 GCGATAGCGG AGTGTATACT GGCTTAACTA TGCGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CGGTGTGAAA TACCGCACAG ATGCGTAAGG
     CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTCGTCTAAC ATGACTCTCA CGTGGTATAC GCCACACTTT ATGGCGTGTC TACGCATTCC

3701 AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG
     TCTTTTATGG CGTAGTCCGC GAGAAGGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCCGCC

3801 TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC
     ATTATGCCAA TAGGTGTCTT AGTCCCCTAT TGCGTCCTTT CTTGTACACT CGTTTTCCGG TCGTTTTCCG GTCCTTGGCA TTTTTCCGGC GCAACGACCG

3901 GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT
     CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGCTGTCCTG ATATTTCTAT GGTCCGCAAA

4001 CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA
     GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTCGCACCGC GAAAGAGTAT

4101 GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG
     CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACACG TGCTTGGGGG GCAAGTCGGG CTGGCGACGC GGAATAGGCC

4201 TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT
     ATTGATAGCA GAACTCAGGT TGGGCCATTC TGTGCTGAAT AGCGGTGACC GTCGTCGGTG ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA
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FIG._ 32E

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4301 ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG
     TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG ACGCGAGACG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC

4401 GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC
     CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTTCG TCGTCTAATG CGCGTCTTTT TTTCCTAGAG TTCTTCTAGG

4501 TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT
     AAACTAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA

4601 TTAAATTAAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA
     AATTTAATTT TTACTTCAAA ATTTAGTTAG ATTTCATATA TACTCATTTG AACCAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT

4701 TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC
     AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG CCCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG

4801 GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG CAACTTTATC CGCCTCCATC
     CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG GCTCGCGTCT TCACCAGGAC GTTGAAATAG GCGGAGGTAG

4901 CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT
     GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAACGCG TTGCAACAAC GGTAACGACG TCCGTAGCAC CACAGTGCGA

5001 CGTCGTTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC
     GCAGCAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG

5101 TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT
     AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA CGTATTAAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA

5201 TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC
     AGACACTGAC CACTCATGAG TTGGTTCAGT AAGACTCTTA TCACATACGC CGCTGGCTCA ACGAGAACGG GCCGCAGTTG TGCCCTATTA TGGCGCGGTG
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FIG._32F

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5301 ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACTCTCAA GGATCTTACC GCTGTTGAGA TCCAGTTCGA TGTAACCCAC
     TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTTGAGAGTT CCTAGAATGG CGACAACTCT AGGTCAAGCT ACATTGGGTG

5401 TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTCACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG
     AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAAGAC CCACTCGTTT TTGTCCTTCC GTTTTACGGC GTTTTTTCCC TTATTCCCGC

5501 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG GGTTATTGTC TCATGAGCGG ATACATATTT GAATGTATTT
     TGTGCCTTTA CAACTTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAAATAGTC CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA

5601 AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG AAAAGTGCCA CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG
     TCTTTTTATT TGTTTATCCC CAAGGCGCGT GTAAAGGGGC TTTTCACGGT GGACTGCAGA TTCTTTGGTA ATAATAGTAC TGTAATTGGA TATTTTTATC

5701 GCGTATCACG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGGAGCT
     CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTCAC TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA

5801 CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC
     GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCAAAGGTGA ACTGTGAAAC TAGGGACTAC CTTTTGCGTA TTAGACCCTG

5901 AGTAGAAAGG GCTTCATCAT ATCAAATGCA ACGTACAAAG AAATAGGGCT TCTGACCTGT GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAAACTATC
     TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTTATCCCGA AGACTGGACA CTTCGTTGTC AGTTACCCGT AAACATATTC TGTTTGATAG

6001 TCACACATCG ACAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAAT CCCCGAAATT ATACACATGA CTGAAGGAAG GGAGCTCGTC
     AGTGTGTAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAAG CATCTCTACA TGTCACTTTA GGGGCTTTAA TATGTGTACT GACTTCCTTC CCTCGAGCAG

6101 ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC ACTTTGATCC CTGATGGAAA ACGCATAATC TGGGACAGTA
     TAAGGGACGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTTTCAA AGGTGAACTG TGAAACTAGG GACTACCTTT TGCGTATTAG ACCCTGTCAT

6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAAGAAAT AGGGCTTCTG ACCTGTGAAG CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC
     CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTTTCTTTA TCCCGAAGAC TGGACACTTC GTTGTCAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG

6301 ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAAATCC CCGAAATTAT ACACATGACT GAAGGAAGGG AGCTCGTCAT
     TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAAGCA TCTCTACATG TCACTTTAGG GGCTTTAATA TGTGTACTGA CTTCCTTCCC TCGAGCAGTA

6401 TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTTACTTTA AAAAAGTTTC CACTTGACAC TTTGATCCCT GATGGAAAAC GCATAATCTG GGACAGTAGA
     AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACTGTG AAACTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCATCT

6501 AAGGGCTTCA TCATATCAAA TGCAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC
     TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCGT TGTCAGTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG

6601 ATCGACAAAC CAATACAATC
     TAGCTGTTTG GTTATGTTAG
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FIG._32G

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  1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC
    AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCAATAATTA TCATTAGTTA ATGCCCCAGT AATCAAGTAT CGGGTATATA CCTCAAGGCG CAATGTATTG

101 TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA
    AATGCCATTT ACCGGGCGGA CCGACTGGCG GGTTGCTGGG GGCGGGTAAC TGCAGTTATT ACTGCATACA AGGGTATCAT TGCGGTTATC CCTGAAAGGT

201 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT
    AACTGCAGTT ACCCACCTCA TAAATGCCAT TTGACGGGTG AACCGTCATG TAGTTCACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA

301 AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC
    TTTACCGGGC GGACCGTAAT ACGGGTCATG TACTGGAATA CCCTGAAAGG ATGAACCGTC ATGTAGATGC ATAATCAGTA GCGATAATGG TACCACTACG

401 GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA
    CCAAAACCGT CATGTAGTTA CCCGCACCTA TCGCCAAACT GAGTGCCCCT AAAGGTTCAG AGGTGGGGTA ACTGCAGTTA CCCTCAAACA AAACCGTGGT

501 AAATCAACGG GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTCGT
    TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAGGCGG GGTAACTGCG TTTACCCGCC ATCCGCACAT GCCACCCTCC AGATATATTC GTCTCGAGCA

601 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT CCATAGAAGA CACCGGGACC GATCCAGCCT CCGCGGCCGG GAACGGTGCA
    AATCACTTGG CAGTCTAGCG GACCTCTGCG GTAGGTGCGA CAAAACTGGA GGTATCTTCT GTGGCCCTGG CTAGGTCGGA GGCGCCGGCC CTTGCCACGT

701 TTGGAACGCG GATTCCCCGT GCCAAGAGTG ACGTAAGTAC CGCCTATAGA GTCTATAGGC CCACCCCCTT GGCTTCGTTA GAACGCGGCT ACAATTAATA
    AACCTTGCGC CTAAGGGGCA CGGTTCTCAC TGCATTCATG GCGGATATCT CAGATATCCG GGTGGGGGAA CCGAAGCAAT CTTGCGCCGA TGTTAATTAT

801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACTCCCAG GTCCAACTGC
    GTATTGGAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CGGAAAGAGA GGTGTCCACA GGTGAGGGTC CAGGTTGACG

901 ACCTCGGTTC TATCGATTGA ATTCCACCAT GGGATGGTCA TGTATCATCC TTTTTCTAGT AGCAACTGCA ACTGGAGTAC ATTCAGATAT CCAGATGACC
    TGGAGCCAAG ATAGCTAACT TAAGGTGGTA CCCTACCAGT ACATAGTAGG AAAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG
  1                                  M   G  W  S   C  I  I  L   F  L  V   A  T  A   T  G  V  H   S  D  I   Q  M  T
                                     ^met                                                          ^Start VL
                                                                                                      ^EcoRV
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FIG._33A

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1001 CAGTCCCCGA GCTCCCTGTC CGCCTCTGTG GGCGATAGGG TCACCATCAC CTGCCGTGCC AGTCAGGATG TGTCCACTGC TGTAGCCTGG TATCAACAGA
     GTCAGGGGCT CGAGGGACAG GCGGAGACAC CCGCTATCCC AGTGGTAGTG GACGGCACGG TCAGTCCTAC ACAGGTGACG ACATCGGACC ATAGTTGTCT
  25 Q  S  P  S   S  L  S   A  S  V   G  D  R  V   T  I  T   C  R  A   S  Q  D  V   S  T  A   V  A  W   Y  Q  Q  K
                                                               ^CDR-L1

1101 AACCAGGAAA AGCTCCGAAG CTTCTGATTT ACTCGGCATC CTTCCTCTAC TCTGGAGTCC CTTCTCGCTT CTCTGGTAGC GGTTCCGGGA CGGATTTCAC
     TTGGTCCTTT TCGAGGCTTC GAAGACTAAA TGAGCCGTAG GAAGGAGATG AGACCTCAGG GAAGAGCGAA GAGACCATCG CCAAGGCCCT GCCTAAAGTG
  59  P  G  K   A  P  K   L  L  I  Y   S  A  S   F  L  Y   S  G  V  P   S  R  F   S  G  S   G  S  G  T   D  F  T
                                     ^CDR-L2

1201 TCTGACCATC AGCAGTCTGC AGCCGGAAGA CTTCGCAACT TATTACTGTC AGCAATCTTA TACTACTCCT CCCACGTTCG GACAGGGTAC CAAGGTGGAG
     AGACTGGTAG TCGTCAGACG TCGGCCTTCT GAAGCGTTGA ATAATGACAG TCGTTAGAAT ATGATGAGGA GGGTGCAAGC CTGTCCCATG GTTCCACCTC
  92 L  T  I   S  S  L  Q   P  E  D   F  A  T   Y  Y  C  Q   Q  S  Y   T  T  P   P  T  F  G   Q  G  T   K  V  E
                                                         ^CDR-L3                              ^KpnI

1301 ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCTTCTGT TGTGTGCCTG CTGAATAACT
     TAGTTTGCTT GACACCGACG TGGTAGACAG AAGTAGAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT GACGAAGACA ACACACGGAC GACTTATTGA
 125 I  K  R  T   V  A  A   P  S  V   F  I  F  P   P  S  D   E  Q  L   K  S  G  T   A  S  V   V  C  L   L  N  N  F
         ^start human kappa

 401 TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC
     AGATAGGGTC TCTCCGGTTT CATGTCACCT TCCACCTATT GCGGGAGGTT AGCCCATTGA GGGTCCTCTC ACAGTGTCTC GTCCTGTCGT TCCTGTCGTG
 159  Y  P  R   E  A  K   V  Q  W  K   V  D  N   A  L  Q   S  G  N  S   Q  E  S   V  T  E   Q  D  S  K   D  S  T

 501 CTACAGCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC
     GATGTCGGAG TCGTCGTGGG ACTGCGACTC GTTTCGTCTG ATGCTCTTTG TGTTTCAGAT GCGGACGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG
 192 Y  S  L   S  S  T  L   T  L  S   K  A  D   Y  E  K  H   K  V  Y   A  C  E   V  T  H  Q   G  L  S   S  P  V

 601 ACAAAGAGCT TCAACAGGGG AGAGTGTTAA GCTTGGCCGC CATGGCCCAA CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA
     TGTTTCTCGA AGTTGTCCCC TCTCACAATT CGAACCGGCG GTACCGGGTT GAACAAATAA CGTCGAATAT TACCAATGTT TATTTCGTTA TCGTAGTGTT
 225 T  K  S  F   N  R  G   E  C  O
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FIG._ 33B

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1701 ATTTCACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC AAACTCATCA ATGTATCTTA TCATGTCTGG ATCGGGAATT AATTCGGCGC
     TAAAGTGTTT ATTTCGTAAA AAAAGTGACG TAAGATCAAC ACCAAACAGG TTTGAGTAGT TACATAGAAT AGTACAGACC TAGCCCTTAA TTAAGCCGCG

1801 AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACTTGG TTAGGTATCT TCTGAGGCGG AAAGAACCAG CTGTGGAATG TGTGTCAGTT AGGGTGTGGA
     TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATAGA AGACTCCGCC TTTCTTGGTC GACACCTTAC ACACAGTCAA TCCCACACCT
                                                                  ^change from C to T, kill KpnI site

1901 AAGTCCCCAG GCTCCCCAGC AGGCAGAAGT ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGCAGAA
     TTCAGGGGTC CGAGGGGTCG TCCGTCTTCA TACGTTTCGT ACGTAGAGTT AATCAGTCGT TGGTCCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGTCTT

2001 GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCCTA ACTCCGCCCA TCCCGCCCCT AACTCCGCCC AGTTCCGCCC ATTCTCCGCC
     CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGAT TGAGGCGGGT AGGGCGGGGA TTGAGGCGGG TCAAGGCGGG TAAGAGGCGG

2101 CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCCGAG GCCGCCTCGG CCTCTGAGCT ATTCCAGAAG TAGTGAGGAG GCTTTTTTGG AGGCCTAGGC
     GGTACCGACT GATTAAAAAA AATAAATACG TCTCCGGCTC CGGCGGAGCC GGAGACTCGA TAAGGTCTTC ATCACTCCTC CGAAAAAACC TCCGGATCCG

2201 TTTTGCAAAA AGCTGTTAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA
     AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AAATGTTGCA GCACTGACCC TTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTGT

2301 TCCCCCCTTC GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGTAGC CTGAATGGCG AATGGCGCCT GATGCGGTAT
     AGGGGGGAAG CGGTCGACCG CATTATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGGTTGT CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA

2401 TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GTCAAAGCAA CCATAGTACG CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT
     AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCGTT GGTATCATGC GCGGGACATC GCCGCGTAAT TCGCGCCGCC CACACCACCA

2501 TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA
     ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGGATCGC GGGCGAGGAA AGCGAAAGAA GGGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT

2601 GCTCTAAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC AAAAAACTTG ATTTGGGTGA TGGTTCACGT AGTGGGCCAT
     CGAGATTTAG CCCCCGAGGG AAATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGGG TTTTTTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA
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FIG._ 33 C

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2701 CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTTCCA AACTGGAACA ACACTCAACC CTATCTCGGG
     GCGGGACTAT CTGCCAAAAA GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG AGAACAAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC

2801 CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA AAAATGAGCT GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA
     GATAAGAAAA CTAAATATTC CCTAAAACGG CTAAAGCCGG ATAACCAATT TTTTACTCGA CTAAATTGTT TTTAAATTGC GCTTAAAATT GTTTTATAAT

2901 ACGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC
     TGCAAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG GTTGAGGCGA TAGCGATGCA CTGACCCAGT ACCGACGCGG

3001 CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT
     GGCTGTGGGC GGTTGTGGGC GACTGCGCGG GACTGCCCGA ACAGACGAGG GCCGTAGGCG AATGTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA

3101 CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGT ATTCTTGAAG ACGAAAGGGC CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA
     GTCTCCAAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCTTTCCCG GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT

3201 TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT
     ATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCCTTT ACACGCGCCT TGGGGATAAA CAAATAAAAA GATTTATGTA AGTTTATACA TAGGCGAGTA

3301 GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT
     CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAGT TGTAAAGGCA CAGCGGGAAT AAGGGAAAAA ACGCCGTAAA

3401 TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA
     ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACTTTC ATTTTCTACG ACTTCTAGTC AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT

3501 GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC
     CGCCATTCTA GGAACTCTCA AAAGCGGGGC TTCTTGCAAA AGGTTACTAC TCGTGAAAAT TTCAAGACGA TACACCGCGC CATAATAGGG CACTACTGCG

3601 CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA
     GCCCGTTCTC GTTGAGCCAG CGGCGTATGT GATAAGAGTC TTACTGAACC AACTCATGAG TGGTCAGTGT CTTTTCGTAG AATGCCTACC GTACTGTCAT
```

FIG._ 33 D

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3701 AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC
     TCTCTTAATA CGTCACGACG GTATTGGTAC TCACTATTGT GACGCCGGTT GAATGAAGAC TGTTGCTAGC CTCCTGGCTT CCTCGATTGG CGAAAAAACG

3801 ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT
     TGTTGTACCC CCTAGTACAT TGAGCGGAAC TAGCAACCCT TGGCCTCGAC TTACTTCGGT ATGGTTTGCT GCTCGCACTG TGGTGCTACG GTCGTCGTTA

3901 GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA
     CCGTTGTTGC AACGCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT TAATTATCTG ACCTACCTCC GCCTATTTCA ACGTCCTGGT

4001 CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG
     GAAGACGCGA GCCGGGAAGG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCCGGTCTAC

4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA
     CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCCTC AGTCCGTTGA TACCTACTTG CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT

4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT
     CGTAACCATT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT AAAAATTAAA TTTTCCTAGA TCCACTTCTA GGAAAAACTA

4301 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTTCTGC
     TTAGAGTACT GGTTTTAGGG AATTGCACTC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT CTTTTCTAGT TTCCTAGAAG AACTCTAGGA AAAAAAGACG

4401 GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT
     CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAAACGGCC TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA

4501 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
     GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGGTGAA GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT

4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
     TAGGACAATG GTCACCGACG ACGGTCACCG CTATTCAGCA CAGAATGGCC CAACCTGAGT TCTGCTATCA ATGGCCTATT CCGCGTCGCC AGCCCGACTT
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FIG._33E

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4701 CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG
     GCCCCCCAAG CACGTGTGTC GGGTCGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG ATGTCGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC

4801 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC
     CTCTTTCCGC CTGTCCATAG GCCATTCGCC GTCCCAGCCT TGTCCTCTCG CGTGCTCCCT CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG

4901 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC
     CCCAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCCGCCTCG GATACCTTTT TGCGGTCGTT GCGCCGGAAA AATGCCAAGG

5001 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG
     ACCGGAAAAC GACCGGAAAA CGAGTGTACA AGAAAGGACG CAATAGGGGA CTAAGACACC TATTGGCATA ATGGCGGAAA CTCACTCGAC TATGGCGAGC

5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA
     GGCGTCGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCTTC TCGCGGGTTA TGCGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT

5201 TCCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTACC TCACTCATTA GGCACCCCAG GCTTTACACT
     AGGTCGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

5301 TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTAA
     AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAATT
```

FIG._33F

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  1 ATTCGAGCTC GCCCGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA
    TAAGCTCGAG CGGGCTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT

101 CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC
    GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAAGG

201 ATTGACGTCA ATGGGTGGAG TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG
    TAACTGCAGT TACCCACCTC ATAAATGCCA TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG GGATAACTGC AGTTACTGCC

301 TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG
    ATTTACCGGG CGGACCGTAA TACGGGTCAT GTACTGGAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC

401 CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC
    GCCAAAACCG TCATGTAGTT ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT ACCCTCAAAC AAAACCGTGG

501 AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG
    TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC

601 TTTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCCG GGAACGGTGC
    AAATCACTTG GCAGTCTAGC GGACCTCTGC GGTAGGTGCG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCCGGC CCTTGCCACG

701 ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG AGTCTATAGG CCCACCCCCT TGGCTTCGTT AGAACGCGGC TACAATTAAT
    TAACCTTGCG CCTAAGGGGC ACGGTTCTCA CTGCATTCAT GGCGGATATC TCAGATATCC GGGTGGGGGA ACCGAAGCAA TCTTGCGCCG ATGTTAATTA

801 ACATAACCTT ATGTATCATA CACATACGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCCTTTCTC TCCACAGGTG TCCACTCCCA GGTCCAACTG
    TGTATTGGAA TACATAGTAT GTGTATGCTA AATCCACTGT GATATCTTAT TGTAGGTGAA ACGGAAAGAG AGGTGTCCAC AGGTGAGGGT CCAGGTTGAC

901 CACCTCGGTT CTATCGATTG AATTCCACCA TGGGATGGTC ATGTATCATC CTTTTTCTAG TAGCAACTGC AACTGGAGCG TACGCTGAGG TTCAGCTGGT
    GTGGAGCCAA GATAGCTAAC TTAAGGTGGT ACCCTACCAG TACATAGTAG GAAAAAGATC ATCGTTGACG TTGACCTCGC ATGCGACTCC AAGTCGACCA
  1                                M   G  W  S   C  I  I   L  F  L  V   A  T  A   T  G  A   Y  A  E  V   Q  L  V
                                   ^start signal peptide                                    ^start of heavy chain
                                   ^met                                                          ^BsiW1
```

FIG._34A

```
1001 GGAGTCTGGC GGTGGCCTGG TGCAGCCAGG GGGCTCACTC CGTTTGTCCT GTGCAGCTTC TGGCTTCACC ATTAGTGGTT CTTGGATACA CTGGGTGCGT
     CCTCAGACCG CCACCGGACC ACGTCGGTCC CCCGAGTGAG GCAAACAGGA CACGTCGAAG ACCGAAGTGG TAATCACCAA GAACCTATGT GACCCACGCA
  25   E  S  G   G  G  L  V   Q  P  G   G  S  L   R  L  S  C   A  A  S   G  F  T   I  S  G  S   W  I  H   W  V  R
                                                                     ^CDR-H1

1101 CAGGCCCCGG GTAAGGGCCT GGAATGGGTT GCTTGGATTG CTCCTTATAG CGGCGCTACT GACTATGCCG ATAGCGTCAA GGGCCGTTTC ACTATAAGCG
     GTCCGGGGCC CATTCCCGGA CCTTACCCAA CGAACCTAAC GAGGAATATC GCCGCGATGA CTGATACGGC TATCGCAGTT CCCGGCAAAG TGATATTCGC
  58  Q  A  P   G  K  G  L   E  W  V   A  W  I   A  P  Y  S   G  A  T   D  Y  A   D  S  V  K   G  R  F   T  I  S   A
                                       ^CDR-H2

1201 CAGACACATC CAAAAACACA GCCTACCTAC AAATGAACAG CTTAAGAGCT GAGGACACTG CCGTCTATTA TTGTGCAAGA GAGGGGGGCT TGTACTGGGT
     GTCTGTGTAG GTTTTTGTGT CGGATGGATG TTTACTTGTC GAATTCTCGA CTCCTGTGAC GGCAGATAAT AACACGTTCT CTCCCCCCGA ACATGACCCA
  92    D  T  S   K  N  T   A  Y  L  Q   M  N  S   L  R  A   E  D  T  A   V  Y  Y   C  A  R   E  G  G  L   Y  W  V
                                                                                               ^CDR-H3

1301 GTTCGACTAC TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT
     CAAGCTGATG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGGAGGT GGTTCCCGGG TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTCGTGGAGA
 125   F  D  Y   W  G  Q  G   T  L  V   T  V  S   S  A  S  T   K  G  P   S  V  F   P  L  A  P   S  S  K   S  T  S
                                                                            ^Apa1

1401 GGGGGCACAG CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG TCGTGGAACT CAGGCGCCCT GACCAGCGGC GTGCACACCT
     CCCCCGTGTC GCCGGGACCC GACGGACCAG TTCCTGATGA AGGGGCTTGG CCACTGCCAC AGCACCTTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA
 158  G  G  T   A  A  L  G   C  L  V   K  D  Y   F  P  E  P   V  T  V   S  W  N   S  G  A  L   T  S  G   V  H  T   F

1501 TCCCGGCTGT CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACTGTGCCCT CTAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA
     AGGGCCGACA GGATGTCAGG AGTCCTGAGA TGAGGGAGTC GTCGCACCAC TGACACGGGA GATCGTCGAA CCCGTGGGTC TGGATGTAGA CGTTGCACTT
 192    P  A  V   L  Q  S   S  G  L  Y   S  L  S   S  V  V   T  V  P  S   S  S  L   G  T  Q   T  Y  I  C   N  V  N

1601 TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC CAGCACCTGA ACTCCTGGGG
     AGTGTTCGGG TCGTTGTGGT TCCACCTGTT CTTTCAACTC GGGTTTAGAA CACTGTTTTG AGTGTGTACG GGTGGCACGG GTCGTGGACT TGAGGACCCC
 225   H  K  P   S  N  T  K   V  D  K   K  V  E   P  K  S  C   D  K  T   H  T  C   P  P  C  P   A  P  E   L  L  G
```

FIG._34B

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1701 GGACCGTCAG TCTTCCTCTT CCCCCCAAAA CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCCACGAAG
     CCTGGCAGTC AGAAGGAGAA GGGGGGTTTT GGGTTCCTGT GGGAGTACTA GAGGGCCTGG GGACTCCAGT GTACGCACCA CCACCTGCAC TCGGTGCTTC
 258 G  P  S  V   F  L  F   P  P  K   P  K  D  T   L  M  I   S  R  T   P  E  V  T   C  V  V   V  D  V   S  H  E  D

1801 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT
     TGGGACTCCA GTTCAAGTTG ACCATGCACC TGCCGCACCT CCACGTATTA CGGTTCTGTT TCGGCGCCCT CCTCGTCATG TTGTCGTGCA TGGCCCACCA
 292  P  E  V   K  F  N   W  Y  V  D   G  V  E   V  H  N   A  K  T  K   P  R  E   E  Q  Y   N  S  T  Y   R  V  V

1901 CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA GAAAACCATC
     GTCGCAGGAG TGGCAGGACG TGGTCCTGAC CGACTTACCG TTCCTCATGT TCACGTTCCA GAGGTTGTTT CGGGAGGGTC GGGGGTAGCT CTTTTGGTAG
 325 S  V  L   T  V  L  H   Q  D  W   L  N  G   K  E  Y  K   C  K  V   S  N  K   A  L  P  A   P  I  E   K  T  I

2001 TCCAAAGCCA AAGGGCAGCC CCGAGAACCA CAGGTGTACA CCCTGCCCCC ATCCCGGGAA GAGATGACCA AGAACCAGGT CAGCCTGACC TGCCTGGTCA
     AGGTTTCGGT TTCCCGTCGG GGCTCTTGGT GTCCACATGT GGGACGGGGG TAGGGCCCTT CTCTACTGGT TCTTGGTCCA GTCGGACTGG ACGGACCAGT
 358 S  K  A  K   G  Q  P   R  E  P   Q  V  Y  T   L  P  P   S  R  E   E  M  T  K   N  Q  V   S  L  T   C  L  V  K

2101 AAGGCTTCTA TCCCAGCGAC ATCGCCGTGG AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC GTGCTGGACT CCGACGGCTC
     TTCCGAAGAT AGGGTCGCTG TAGCGGCACC TCACCCTCTC GTTACCCGTC GGCCTCTTGT TGATGTTCTG GTGCGGAGGG CACGACCTGA GGCTGCCGAG
 392  G  F  Y   P  S  D   I  A  V  E   W  E  S   N  G  Q   P  E  N  N   Y  K  T   T  P  P   V  L  D  S   D  G  S

2201 CTTCTTCCTC TACAGCAAGC TCACCGTGGA CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG AGGCTCTGCA CAACCACTAC
     GAAGAAGGAG ATGTCGTTCG AGTGGCACCT GTTCTCGTCC ACCGTCGTCC CCTTGCAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTTGGTGATG
 425 F  F  L   Y  S  K  L   T  V  D   K  S  R   W  Q  Q  G   N  V  F   S  C  S   V  M  H  E   A  L  H   N  H  Y

2301 ACGCAGAAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCCTA GAGTCGACCT GCAGAAGCTT GGCCGCCATG GCCCAACTTG TTTATTGCAG
     TGCGTCTTCT CGGAGAGGGA CAGAGGCCCA TTTACTCACG CTGCCGGGAT CTCAGCTGGA CGTCTTCGAA CCGGCGGTAC CGGGTTGAAC AAATAACGTC
 458 T  Q  K  S   L  S  L   S  P  G   K  O

2401 CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT
     GAATATTACC AATGTTTATT TCGTTATCGT AGTGTTTAAA GTGTTTATTT CGTAAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA
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FIG._34C

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2501 ATCTTATCAT GTCTGGATCG ATCGGGAATT AATTCGGCGC AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACTTGG TTAGGTACCT TCTGAGGCGG
     TAGAATAGTA CAGACCTAGC TAGCCCTTAA TTAAGCCGCG TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATGGA AGACTCCGCC

2601 AAAGAACCAT CTGTGGAATG TGTGTCAGTT AGGGTGTGGA AAGTCCCCAG GCTCCCCAGC AGGCAGAAGT ATGCAAAGCA TGCATCTCAA TTAGTCAGCA
     TTTCTTGGTA GACACCTTAC ACACAGTCAA TCCCACACCT TTCAGGGGTC CGAGGGGTCG TCCGTCTTCA TACGTTTCGT ACGTAGAGTT AATCAGTCGT

2701 ACCAGGTGTG GAAAGTCCCC AGGCTCCCCA GCAGGCAGAA GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCCGCCCCTA ACTCCGCCCA
     TGGTCCACAC CTTTCAGGGG TCCGAGGGGT CGTCCGTCTT CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGAT TGAGGCGGGT

2801 TCCCGCCCCT AACTCCGCCC AGTTCCGCCC ATTCTCCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCCGAG GCCGCCTCGG CCTCTGAGCT
     AGGGCGGGGA TTGAGGCGGG TCAAGGCGGG TAAGAGGCGG GGTACCGACT GATTAAAAAA AATAAATACG TCTCCGGCTC CGGCGGAGCC GGAGACTCGA

2901 ATTCCAGAAG TAGTGAGGAG GCTTTTTTGG AGGCCTAGGC TTTTGCAAAA AGCTGTTAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG
     TAAGGTCTTC ATCACTCCTC CGAAAAAACC TCCGGATCCG AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AAATGTTGCA GCACTGACCC

3001 AAAACCCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCCTTC GCCAGTTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA
     TTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTGT AGGGGGGAAG CGGTCAACCG CATTATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGGTTGT

3101 GTTGCGTAGC CTGAATGGCG AATGGCGCCT GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GTCAAAGCAA CCATAGTACG
     CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCGTT GGTATCATGC

3201 CGCCCTGTAG CGGCGCATTA AGCGCGGCGG GTGTGGTGGT TACGCGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
     GCGGGACATC GCCGCGTAAT TCGCGCCGCC CACACCACCA ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGGATCGC GGGCGAGGAA AGCGAAAGAA

3301 CCCTTCCTTT CTCGCCACGT TCGCCGGCTT TCCCCGTCAA GCTCTAAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC
     GGGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT CGAGATTTAG CCCCCGAGGG AAATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGGG

3401 AAAAAACTTG ATTTGGGTGA TGGTTCACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC
     TTTTTTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA GCGGGACTAT CTGCCAAAAA GCGGGAAACT GCAACCTCAG GTGCAAGAAA TTATCACCTG
```

FIG._34 D

```
3501 TCTTGTTCCA AACTGGAACA ACACTCAACC CTATCTCGGG CTATTCTTTT GATTTATAAG GGATTTTGCC GATTTCGGCC TATTGGTTAA AAAATGAGCT
     AGAACAAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC GATAAGAAAA CTAAATATTC CCTAAAACGG CTAAAGCCGG ATAACCAATT TTTTACTCGA

3601 GATTTAACAA AAATTTAACG CGAATTTTAA CAAAATATTA ACGTTTACAA TTTTATGGTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC
     CTAAATTGTT TTTAAATTGC GCTTAAAATT GTTTTATAAT TGCAAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG

3701 CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC
     GTTGAGGCGA TAGCGATGCA CTGACCCAGT ACCGACGCGG GGCTGTGGGC GGTTGTGGGC GACTGCGCGG GACTGCCCGA ACAGACGAGG GCCGTAGGCG

3801 TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCAGT ATTCTTGAAG ACGAAAGGGC
     AATGTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGCTTTCCCG

3901 CTCGTGATAC GCCTATTTTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT
     GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT ATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCCTTT ACACGCGCCT TGGGGATAAA

4001 GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA
     CAAATAAAAA GATTTATGTA AGTTTATACA TAGGCGAGTA CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAAGT

4101 ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG
     TGTAAAGGCA CAGCGGGAAT AAGGGAAAAA ACGCCGTAAA ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACTTTC ATTTTCTACG ACTTCTAGTC

4201 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA
     AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT CGCCATTCTA GGAACTCTCA AAAGCGGGGC TTCTTGCAAA AGGTTACTAC TCGTGAAAAT

4301 AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC
     TTCAAGACGA TACACCGCGC CATAATAGGG CACTACTGCG GCCCGTTCTC GTTGAGCCAG CGGCGTATGT GATAAGAGTC TTACTGAACC AACTCATGAG

4401 ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG
     TGGTCAGTGT CTTTTCGTAG AATGCCTACC GTACTGTCAT TCTCTTAATA CGTCACGACG GTATTGGTAC TCACTATTGT GACGCCGGTT GAATGAAGAC

4501 ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA
     TGTTGCTAGC CTCCTGGCTT CCTCGATTGG CGAAAAAACG TGTTGTACCC CCTAGTACAT TGAGCGGAAC TAGCAACCCT TGGCCTCGAC TTACTTCGGT
```

FIG._34E

```
4601 TACCAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA
     ATGGTTTGCT GCTCGCACTG TGGTGCTACG GTCGTCGTTA CCGTTGTTGC AACGCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT

4701 ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG
     TAATTATCTG ACCTACCTCC GCCTATTTCA ACGTCCTGGT GAAGACGCGA GCCGGGAAGG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC

4801 CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
     GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCCGGTCTAC CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCCTC AGTCCGTTGA TACCTACTTG

4901 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA
     CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTAATT CGTAACCATT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAACTAA ATTTTGAAGT

5001 TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA
     AAAAATTAAA TTTTCCTAGA TCCACTTCTA GGAAAAACTA TTAGAGTACT GGTTTTAGGG AATTGCACTC AAAAGCAAGG TGACTCGCAG TCTGGGGCAT

5101 GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGTTTGCCGG
     CTTTTCTAGT TTCCTAGAAG AACTCTAGGA AAAAAGACG CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAAACGGCC

5201 ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT
     TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGGTGAA

5301 CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA
     GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT TAGGACAATG GTCACCGACG ACGGTCACCG CTATTCAGCA CAGAATGGCC CAACCTGAGT

5401 AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC
     TCTGCTATCA ATGGCCTATT CCGCGTCGCC AGCCCGACTT GCCCCCCAAG CACGTGTGTC GGGTCGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG

5501 TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA
     ATGTCGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC CTCTTTCCGC CTGTCCATAG GCCATTCGCC GTCCCAGCCT TGTCCTCTCG CGTGCTCCCT

601 GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC
    CGAAGGTCCC CCTTTGCGGA CCATAGAAAT ATCAGGACAG CCCAAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCCGCCTCG
```

FIG._34F

```
5701 CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG
     GATACCTTTT TGCGGTCGTT GCGCCGGAAA AATGCCAAGG ACCGGAAAAC GACCGGAAAA CGAGTGTACA AGAAAGGACG CAATAGGGGA CTAAGACACC

5801 ATAACCGTAT TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT
     TATTGGCATA ATGGCGGAAA CTCACTCGAC TATGGCGAGC GGCGTCGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCTTC TCGCGGGTTA

5901 ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TCCAACTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT
     TGCGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT AGGTTGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA

6001 GTGAGTTACC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
     CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT

6101 ACAGCTATGA CCATGATTAC GAATTA
     TGTCGATACT GGTACTAATG CTTAAT
```

FIG._34G

LC Frequency

28	S	N	V	D	G	I	T	L	X			
	511	262	258	186	178	44	39	16	35			
29	I	S	V	G	N	X						
	612	272	254	192	147	70						
30	S	N	K	G	R	Y	T	D	A	X		
	849	176	169	86	81	63	29	28	17	45		
31	S	N	T	R	I	D	K	G	X			
	676	496	170	47	29	28	25	18	53			
32	Y	N	W	F	S	D	R	X				
	1055	128	97	77	61	40	25	69				
50	G	A	D	W	K	L	E	S	X			
	386	341	294	151	116	91	39	30	82			
53	S	N	T	K	I	R	X					
	545	438	407	41	23	23	58					
91	Y	S	R	A	G	H	X					
	849	196	169	118	61	41	148					
92	Y	G	N	S	D	L	T	H	I	X		
	362	356	248	193	114	94	64	43	38	91		
93	S	N	Q	T	H	G	D	R	X			
	738	346	117	101	66	51	47	35	112			
94	S	T	W	Y	L	F	A	P	V	I	N	X
	386	365	288	172	114	79	46	43	33	24	18	40
96	L	Y	W	F	I	R	P	X				
	264	205	176	140	117	115	46	121				

FIG._35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIIK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

FIG._36

Light Chain Designed Diversity
Diversity: ~ 2.9×10^9

CDR-L1: diversity ~ 7×10^3

28 RDT	29 RTT	30 RVW	31 RVW	32 DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

CDR-L2: diversity = 18

50 KBG	53 AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity ~ 2.3×10^4

91 KMT	92 DHT	93 DHT	94 NHT	96 YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			Y	

FIG._37

Light Chain Designed Diversity
Diversity: ~ 6.1×10^8

CDR-L1: diversity ~ 3.4×10^3

28 RDT	29 RTT	30 RVW	31 ANW	32 THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T		
		V		

CDR-L2: diversity = 18

50 KBG	53 AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity ~ 1.0×10^4

91 KMT	92 DMC	93 RVT	94 NHT	96 YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

FIG._38

Light Chain Designed Diversity

CDR-L3: diversity ~ 1.3×10^3

91	92	93	94	96
TMT	DMC	RVT	WHT	HTT
S	A	A	F	F
Y	D	D	I	I
	N	G	N	L
	S	N	S	
	T	S	T	
	Y	T	Y	

FIG._39

CDR-L1

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		V	V	V
				Y

CDR-L2

50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

CDR-L3

91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

*Amber stop codon is encoded by the degenerate codon

FIG._40

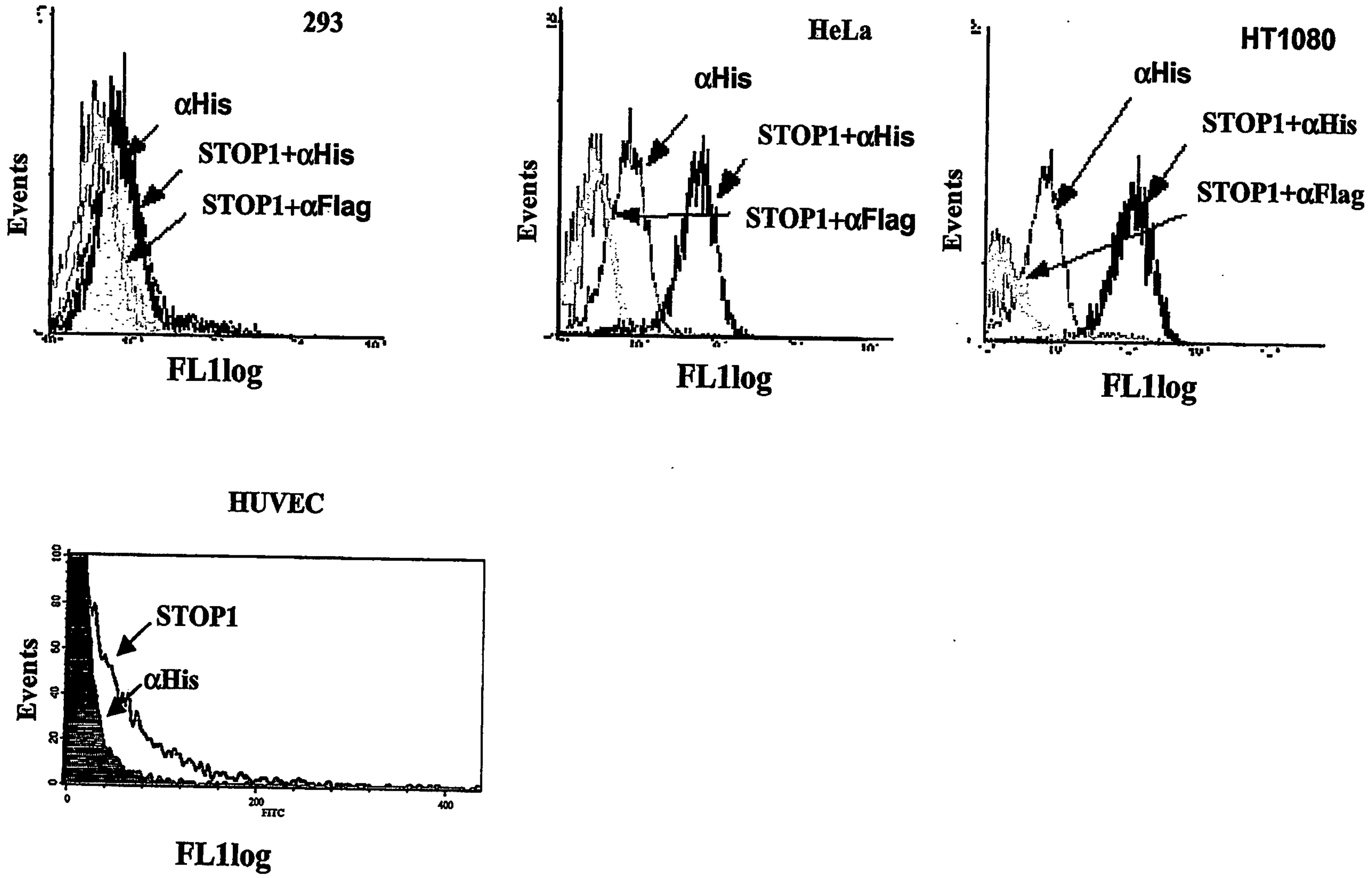

293
αHis
STOP1+αHis
STOP1+αFlag
Events
FL1log
HeLa
αHis
STOP1+αHis
STOP1+αFlag
Events
FL1log
HT1080
αHis
STOP1+αHis
STOP1+αFlag
Events
FL1log
HUVEC
STOP1
αHis
Events
0
20
40
60
80
100
0
200
400
FITC
FL1log

FIG.41

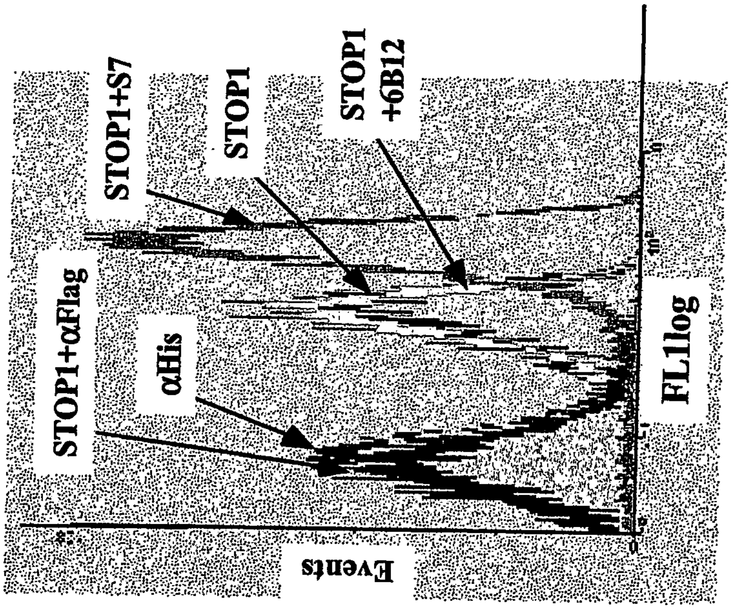


FIG.42

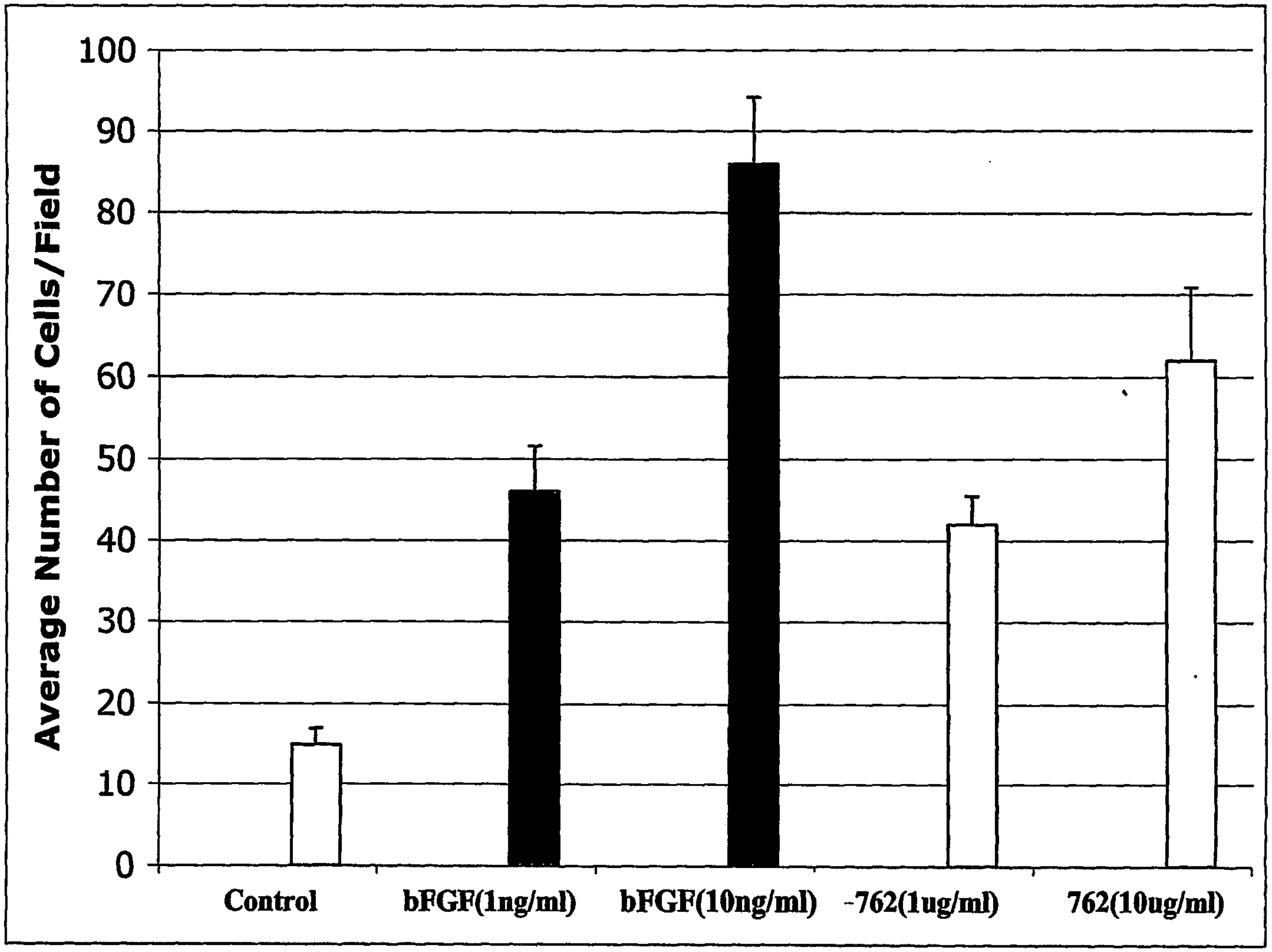
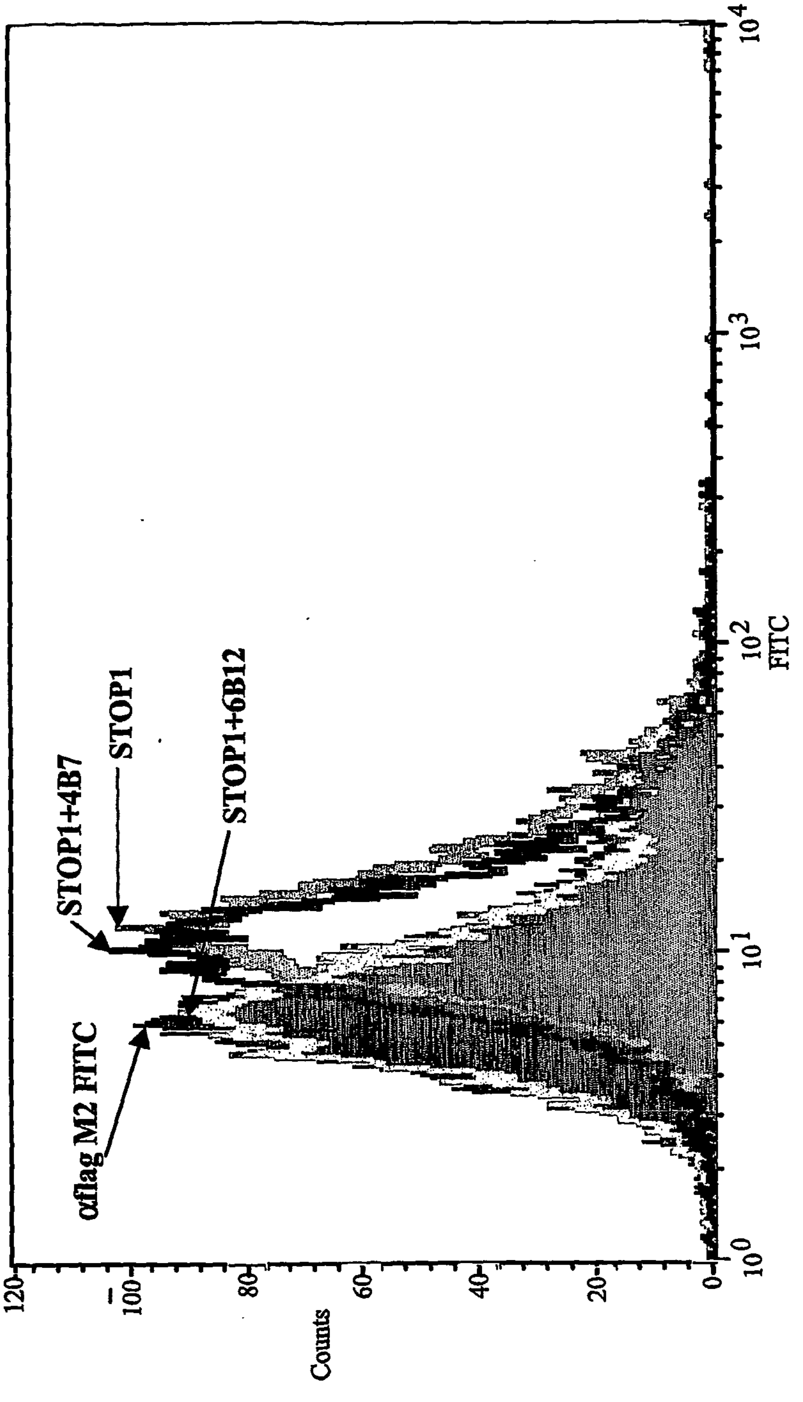

Average Number of Cells/Field
100
90
80
70
60
50
40
30
20
10
0
Control
bFGF(1ng/ml)
bFGF(10ng/ml)
762(1ug/ml)
762(10ug/ml)

FIG.43



αflag M2 FITC
STOP1+4B7
STOP1
STOP1+6B12
Counts
120
100
80
60
40
20
0
10^0
10^1
10^2
10^3
10^4
FITC

FIG.44

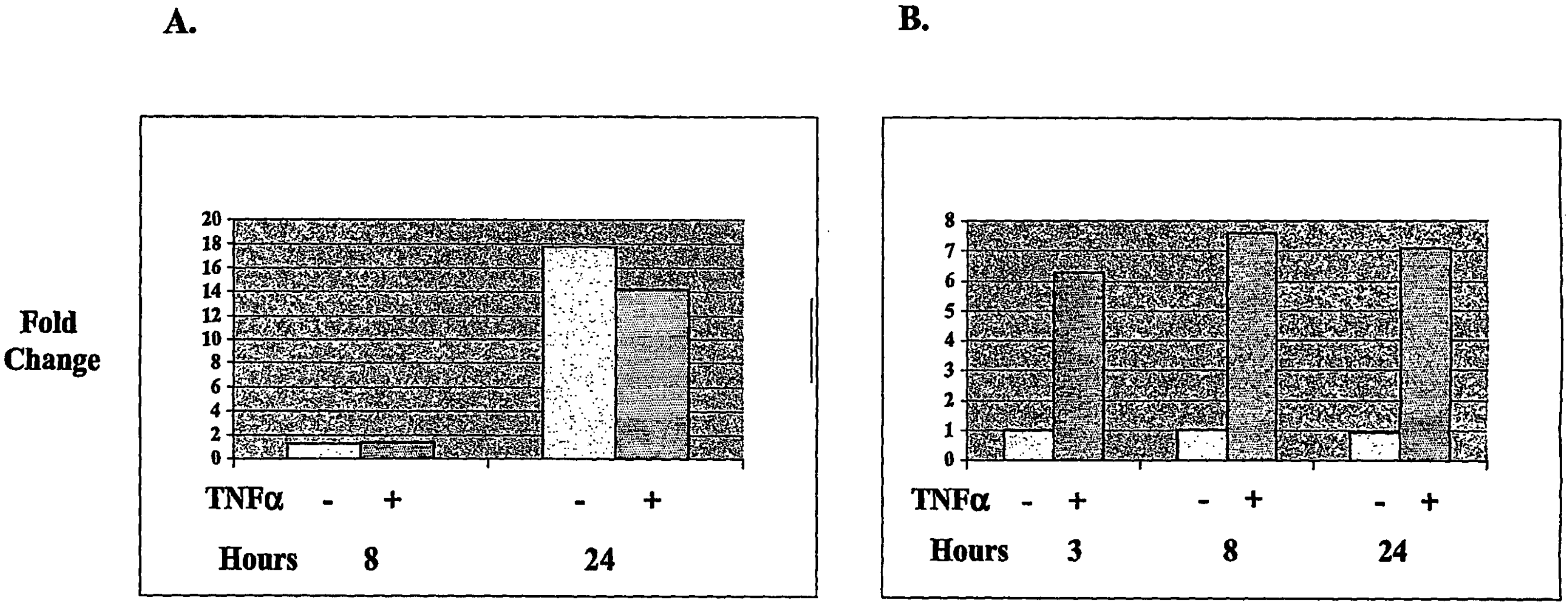

A.
B.
Fold
Change
20
18
16
14
12
10
8
6
4
2
0
TNFα - + - +
Hours 8 24
8
7
6
5
4
3
2
1
0
TNFα - + - + - +
Hours 3 8 24

FIG.45

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